

## SEQUENCE LISTING

- <110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350  
<141> 2000-09-18
- <150> PCT/US00/04414  
<151> 2000-02-22
- <150> US 60/143,048  
<151> 1999-07-07
- <150> US 60/145,698  
<151> 1999-07-26
- <150> US 60/146,222  
<151> 1999-07-28
- <150> PCT/US99/20594  
<151> 1999-09-08
- <150> PCT/US99/20944  
<151> 1999-09-13

<150> PCT/US99/21090  
<151> 1999-09-15

<150> PCT/US99/21547  
<151> 1999-09-15

<150> PCT/US99/23089  
<151> 1999-10-05

<150> PCT/US99/28214  
<151> 1999-11-29

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28564  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/30911  
<151> 1999-12-20

<150> PCT/US99/30999  
<151> 1999-12-20  
<150> PCT/US00/00219  
<151> 2000-01-05

<160> 423

<210> 1  
<211> 1825  
<212> DNA  
<213> Homo sapiens

<400> 1  
actgcacctc ggttctatcg attgaattcc ccgggggatcc tctagagatc cctcgacctc 60  
gaccacgcg tccgggccgg agcagcacgg ccgcaggacc tggagctccg gctgcgtctt 120  
cccgcagcgc taccgcctat gcgcctgccg ccgcggggccg cgctggggct cctgccgctt 180  
ctgctgctgc tgccgcccgc gccggaggcc gccaaagaagc cgacgccctg ccaccgggtg 240  
cgggggctgg tggacaagtt taaccagggg atgggtggaca ccgcaaagaa gaactttggc 300  
ggcggaaca cggcttggga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360  
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420  
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480  
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540  
cccgaactgtc tcgcatgcc a gggcggatcc cagaggccct gcagcgggaa tggccactgc 600  
agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg gtaccagggc 660

```

ccgctgtgca ctgactgcat ggacggctac ttcagctcgc tccggaacga gacccacagc 720
atctgcacag cctgtgacga gtcttgcaag acgtgctcgg gcctgaccaa cagagactgc 780
ggcgagtgtg aagtgggctg ggtgctggac gagggcgctt gtgtggatgt ggacgagtgt 840
gcggccgagc cgctccctg cagcgtcgcg cagttctgta agaacgcaa cggtcctac 900
acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc aggaaactgt 960
aaagagtgtg tctctggcta cgcgaggag caccgacagt gtgcagatgt ggacgagtgc 1020
tcactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccaggaggc 1080
tacgtctgtg tgtgtcctga cggcttcgaa gaaacggaag atgcctgtgt gccgccggca 1140
gaggctgaag ccacagaagg agaaagcccc acacagctgc cctcccgca agacctgtaa 1200
tgtgccggac ttaccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260
ggatgccgtc tcctgcagtg gacagcggcg gggagaggct gcctgctctc taacggttga 1320
ttctcatttg tcccttaaac agctgcattt cttggttgtt cttaaacaga cttgtatatt 1380
ttgatacagt tctttgtaat aaaattgacc attgtaggta atcaggagga aaaaaaaaaa 1440
aaaaaaaaaa aaagggcggc cgcgactcta gactcgacct gcagaagctt ggccgccatg 1500
gccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560
cacaaataaa gcattttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620
atcttatcat gtctggatcg ggaattaatt cggcgcagca ccatggcctg aaataacctc 1680
tgaaagagga acttggttag gtaccttctg aggcggaaaag aaccagctgt ggaatgtgtg 1740
tcagttaggg tgtggaaaag cccagagctc cccagcaggc agaagtatgc aagcatgcat 1800
ctcaattagt cagcaacccta gttttt 1825

```

<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
  1              5              10              15

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
      20              25              30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85              90              95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100              105              110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115              120              125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130              135              140

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300  
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320  
 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
 325 330 335  
 Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp  
 340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

cagggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatacctc tagagatccc 60  
 tcgacctcga cccacgcgtc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120  
 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
 ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gagcagcatg gcccggagga 240



```

gggccttccc tgccgccgcg ctctggctct ggagcatcct cctgtgectg ctggcactgc 300
gggcgagggc cgggccgcgc caggaggaga gcctgtacct atggatcgat gctcaccagg 360
caagagtact cataggattt gaagaagata tccctgattgt ttcagagggg aaaatggcac 420
cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480
attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540
ccttgcgctc cctggataaa ggcatcatgg cagatccaac cgtcaatgtc cctctgctgg 600
gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtcct ggaaaacagg 660
atgggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720
tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780
ggtgccgaaa tggaggcttt tgtaatgaaa gacgcatctg cgagtgtcct gatgggttcc 840
acggacctca ctgtgagaaa gccctttgta cccacgatg tatgaatggg ggactttgtg 900
tgactcctgg tttctgcatc tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960
actgctcaac cacctgcttt aatggaggga cctgtttcta ccctggaaaa tgtatttgcc 1020
ctccaggact agaggagag cagtgtgaaa tcagcaaatg cccacaacc tgctgaaatg 1080
gaggtaaatg cattggtaaa agcaaatgta agtgttccaa aggttaccag ggagacctct 1140
gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaacccaaca 1200
aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaagggtac gaagccagcc 1260
tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgect tcacttaaaa 1320
aggccgagga gcggcgggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380
aaacgtttta agttacacca agttcatagc ctttgttaac ctttcatgtg ttgaatgttc 1440
aaataatgtt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag catgatggta 1560
tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcagggtta 1620
aaattttcag tgtgtagtgt gcagatattt tcaaaattac aatgcattta tgggtgtctgg 1680
gggcagggga acatcagaaa ggtaaattg ggcaaaaatg cgtaagtcac aagaatttgg 1740
atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860
ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttactactgt gtagtggcat 1920
ttaaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980
gcattggctt gaagcaatat aatatattgt aaacaaaaca cagctcttac ctaataaaca 2040
ttttatactg tttgtatgta taaaataaag gtgctgcttt agtttttttg aaaaaaaaaa 2100
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgccgcg gactctagag tcgacctgca 2160
gaagcttggc cgccatggcc caacttgttt attgcagctt ataattg 2206

```

&lt;210&gt; 4

&lt;211&gt; 379

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

```

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
  1                      5                      10                      15

```

```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
                20                      25                      30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
                35                      40                      45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
                50                      55                      60

```

```

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

```

65		70		75		80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln						
		85		90		95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly						
		100		105		110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro						
		115		120		125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln						
		130		135		140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu						
		145		150		155
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr						
		165		170		175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys						
		180		185		190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His						
		195		200		205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys						
		210		215		220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn						
		225		230		235
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys						
		245		250		255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln						
		260		265		270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys						
		275		280		285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu						
		290		295		300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys						
		305		310		315
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His						
		325		330		335
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala						
		340		345		350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
 370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 5

agggagcacg gacagtgtgc agatgtggac gagtgtcac tagca

45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 7

taagtcggc acattacagg tc

22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 8

cccacgatgt atgaatggtg gactttgtgt gactcctggt ttctgcatc

49

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 9  
 aaagacgcat ctgcgagtgt cc 22

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 10  
 tgctgatttc aactgctct ccc 23

<210> 11  
 <211> 2197  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 cggacgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60  
 ggccccagcc cacaccttca ccagggccca ggagccacca tgtggcgatg tccactgggg 120  
 ctactgctgt tgctgccgct ggctggccac ttggctcttg gtgccagca gggctcgtggg 180  
 cgccgggagc tagcacccgg tctgcacctg cggggcatcc gggacgcggg aggccgggtac 240  
 tgccaggagc aggacctgtg ctgccgcggc cgtgccgacg actgtgccct gccctacctg 300  
 ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360  
 ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420  
 ggaggtcgta tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcaacctg 480  
 caggagaaca ggcagtggca tggatggatc agacatgatc aaagccatca accaggggcaa 540  
 ctatggctgg caggctggga accacagcgc cttctggggc atgaccttg atgaggggcat 600  
 tcgctaccgc ctgggcacca tccgcccata ttctctgggtc atgaacatgc atgaaattta 660  
 tacagtgtcg aaccacaggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720  
 caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780  
 agcagctgtg gcatccgata gtgtctcaat ccattctctg ggacacatga cgctgtcct 840  
 gtgcgccag aacctgctgt cttgtgacac ccaccagcag cagggtgcc gcggtggggc 900  
 tctcgatggg gcttgggtgt tctgcgtcg ccgaggggtg gtgtctgacc actgctaccc 960  
 cttctcgggc cgtgaacgag acgaggctgg ccctgcgccc ccctgtatga tgcacagccg 1020  
 agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080  
 caatgacatc taccaggtca ctctgtcta ccgcctcggc tccaacgaca aggagatcat 1140  
 gaaggagctg atggagaatg gccctgtcca agccctcatg gaggtgcatg aggacttctt 1200  
 cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260  
 ccgcgcgcat gggacccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320

```

tggaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggcgagag 1380
gggccacttc cgcacgtgc gcggcgtcaa tgagtgcgac atcgagagct tcgtgctggg 1440
cgtctggggc cgcgtgggca tggaggacat gggcatcac tgaggctgcg ggcaccacgc 1500
ggggtccggc ctgggatcca ggctaagggc cggcggaaga ggccccaatg gggcggtgac 1560
cccagcctcg cccgacagag cccggggcgc aggcgggcgc cagggcgcta atcccggcgc 1620
gggttcgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact ggcggagccc 1680
ccagacctcc cagtggggac ggggcagggc ctggcctggg aagagcacag ctgcagatcc 1740
caggcctctg gcgccccac tcaagactac caaagccagg acacctcaag tctccagccc 1800
caatacccca ccccaatccc gtattctttt tttttttttt ttagacaggg tcttgcctcg 1860
ttgcccaggt tggagtgcag tggcccatca gggctcactg taacctccga ctctggggtt 1920
caagtgacct tcccacctca gcctctcaag tagctgggac tacaggtgca ccaccacacc 1980
tggctaattt ttgtattttt tgtaaagagg ggggtctcac tgtgttgccc aggctgggtt 2040
cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgcgt ggattgcagg 2100
catgagccac tgcaccagc cctgtattct tattcttcag atatttattt ttcttttcac 2160
tgttttaaaa taaaaccaa gtattgataa aaaaaaa 2197

```

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly
  1              5              10              15

```

```

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
      20              25              30

```

```

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35              40              45

```

```

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50              55              60

```

```

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65              70              75              80

```

```

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85              90              95

```

```

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100             105             110

```

```

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115             120             125

```

```

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130             135             140

```

```

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
      145             150             155             160

```

His Asp Pro Gly

<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (33)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (80)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (94)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (144)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (188)  
 <223> a, t, c or g

<400> 13  
 aggctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcgtt gtctcaaatac 60  
 caattctctt gggacacatn acgcctgtcc tttingcccca gaacctgctg tcttgtaacac 120  
 ccaccagcag cagggctgcc gcgntgggcg tctcgatggg gcctggtggt tcttgcgctcg 180  
 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240  
 ccctgcgccc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300  
 tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctctgtcta 360  
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420  
 agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480  
 gccagtgagc cttggggaggc cagagagata ccgccggcat gggaccact cag 533

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15

ggcggatatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg

50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcactgccc tgctgtgcta 60  
ctcctgcaaa gcccagggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120  
gggggagcag tgctggaccg cgcgcacccg cgcagttggc ctccctgaccg tcatcagcaa 180  
aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240  
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgcctgc agccggctgc 300  
cgccatcctt gcgtgctcc ctgcactcgg cctgctgctc tggggaccg gccagctata 360  
ggctctgggg ggccccgctg cagccacac tgggtgtggt gccccaggcc tctgtgccac 420  
tcctcacaga cctggcccag tgggagcctg tcctggttcc tgaggcacat cctaacgcaa 480  
gtctgaccat gtatgtctgc acccctgtcc cccaccctga cctcccatg gccctctcca 540  
ggactccac ccggcagatc agctctagt acacagatcc gcctgcagat ggccccctcca 600  
accctctctg ctgctgttcc catggcccag cattctccac ccttaaccct gtgctcaggc 660  
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc cagggtctggt 720  
ccgtgggtgc ccccgacccc agcaggggac aggcactcag gaggggccag taaaggctga 780  
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840  
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900  
aatggcagcc tgagcacagc gtaggcctt aataaacacc tgttggataa gccaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gccc

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

```

cccacgcgtc cgaacctctc cagcgatggg agccgccgcg ctgctgcccc acctcactct 60
gtgcttacag ctgctgattc tctgctgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcaccg ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacgtt tggcagcccg gttcgcatca aaggggctga 300
gagtgagaag tacatctgta tgaacaagag gggcaagctc atcgggaagc ccagcgggaa 360
gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg ccttcagaa 420
cgcccggcac gagggctggt tcatggcctt cacgcggcag gggcgcccc gccaggcttc 480
ccgcagccgc cagaaccagc gcgaggccca cttcatcaag cgctctacc aaggccagct 540
gcccttcccc aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgccccac 600
ccgccggacc aagcgcacac ggcggcccca gccctcacg tagtctggga ggcagggggc 660
agcagccctt gggccgctc cccaccctt tcccttctta atccaaggac tgggctgggg 720
tggcgggagg ggagccagat ccccgaggga ggaccctgag ggccgcgaag catccagacc 780
cccagctggg aaggggcagg ccggtgcccc aggggcggct ggcacagtgc ccccttcccg 840
gacgggtggc aggccctgga gaggaactga gtgtcacctt gatctcaggc caccagcctc 900
tgccggcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg aaggccttgc 960
agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc tcggatctcc ctcagtctgc 1020
ccccagcccc caaactctc ctggctagac tgtaggaagg gacttttgtt tgtttgtttg 1080
tttcaggaaa aaagaaaggg agagagagga aaatagaggg ttgtocactc ctcacattcc 1140
acgacccagg cctgcacccc acccccaact ccagccccg gaataaaacc attttcttgc 1200

```

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgctgctca nctggtcggt catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg cctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatfff ttttttcttt ttctttttcc caccacattg 240  
 tattttatff ccgacttca gaaatgggccc tacagaccac aaagtggccc agccatgggg 300  
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420  
 gcttgacctc agtgcctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtgc gtgcacacgg 540  
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720  
 gggccttccg ggaggctatt agcctcaaat tgttgttttt gtctaagaat caoctgagca 780  
 gtgtgcctgt tgggcttcct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840  
 ctgtcatatc cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900  
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
 aggaattttc aattgtacgt aattcgtctg cccacctcc tcccgatctc ccaggtagcg 1020  
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

```

aagggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcattctctca 1260
acgtgcggggg tttcatgtgc caaggctctg aacaagtccg ggggatggcc gtcaggggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgacccccgg cctgcctctc ttcaccccag 1380
ccccaagtac agctttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440
gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca tacaaaactca 1620
catgggtgaa aatggggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttgtt 1740
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggctcc ccttttctgc tggcgggctt gatcgggggc gcggtgatat 1920
ttgtgctggt ggtcttctgc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaattggg 2160
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacctgga gcactgccat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacgggtg tactatataa 2400
tgggatttaa aaaaagtgc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaattctt
2479

```

&lt;210&gt; 28

&lt;211&gt; 660

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1                      5                      10                      15

```

```

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
          20                      25                      30

```

```

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
          35                      40                      45

```

```

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
          50                      55                      60

```

```

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
          65                      70                      75                      80

```

```

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
          85                      90                      95

```

```

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
          100                      105                      110

```

```

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
          115                      120                      125

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

				405						410					415			
Val	Thr	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Gln	Leu	Ser	Ile	His	Phe	Val			
			420					425					430					
Asn	Asp	Thr	Ser	Ile	Gln	Val	Ser	Trp	Leu	Ser	Leu	Phe	Thr	Val	Met			
			435				440					445						
Ala	Tyr	Lys	Leu	Thr	Trp	Val	Lys	Met	Gly	His	Ser	Leu	Val	Gly	Gly			
		450				455					460							
Ile	Val	Gln	Glu	Arg	Ile	Val	Ser	Gly	Glu	Lys	Gln	His	Leu	Ser	Leu			
465					470				475						480			
Val	Asn	Leu	Glu	Pro	Arg	Ser	Thr	Tyr	Arg	Ile	Cys	Leu	Val	Pro	Leu			
				485					490					495				
Asp	Ala	Phe	Asn	Tyr	Arg	Ala	Val	Glu	Asp	Thr	Ile	Cys	Ser	Glu	Ala			
			500					505					510					
Thr	Thr	His	Ala	Ser	Tyr	Leu	Asn	Asn	Gly	Ser	Asn	Thr	Ala	Ser	Ser			
		515					520					525						
His	Glu	Gln	Thr	Thr	Ser	His	Ser	Met	Gly	Ser	Pro	Phe	Leu	Leu	Ala			
	530					535					540							
Gly	Leu	Ile	Gly	Gly	Ala	Val	Ile	Phe	Val	Leu	Val	Val	Leu	Leu	Ser			
545					550					555					560			
Val	Phe	Cys	Trp	His	Met	His	Lys	Lys	Gly	Arg	Tyr	Thr	Ser	Gln	Lys			
				565					570					575				
Trp	Lys	Tyr	Asn	Arg	Gly	Arg	Arg	Lys	Asp	Asp	Tyr	Cys	Glu	Ala	Gly			
			580					585					590					
Thr	Lys	Lys	Asp	Asn	Ser	Ile	Leu	Glu	Met	Thr	Glu	Thr	Ser	Phe	Gln			
		595					600					605						
Ile	Val	Ser	Leu	Asn	Asn	Asp	Gln	Leu	Leu	Lys	Gly	Asp	Phe	Arg	Leu			
	610					615					620							
Gln	Pro	Ile	Tyr	Thr	Pro	Asn	Gly	Gly	Ile	Asn	Tyr	Thr	Asp	Cys	His			
625					630					635				640				
Ile	Pro	Asn	Asn	Met	Arg	Tyr	Cys	Asn	Ser	Ser	Val	Pro	Asp	Leu	Glu			
				645					650					655				
His	Cys	His	Thr															
			660															

<210> 29  
 <211> 21  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcggcg gcggagacag aggcagaggc agaagctggg gtcctgcct 60  
cgctccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

gaggaagacc	cgggtggctg	cgccctgccc	tgccttccca	ggcgccggcg	gctgcagcct	180
tgccctctct	gctcgccctg	aaaatggaaa	agatgctcgc	aggctgcttt	ctgctgatcc	240
tcggacagat	cgtcctcctc	cctgcccagg	ccagggagcg	gtcacgtggg	aggtccatct	300
ctaggggcag	acacgctcgg	acccaccgcg	agacggccct	tctggagagt	tctgtgaga	360
acaagcgggc	agacctggtt	ttcatcattg	acagctctcg	cagtgtcaac	acccatgact	420
atgcaaaggt	caaggagttc	atcgtggaca	tcttgcaatt	cttgacatt	ggtcctgatg	480
tcacccgagt	gggctgctc	caatatggca	gcactgtcaa	gaatgagttc	tccctcaaga	540
ccttcaagag	gaagtccgag	gtggagcgtg	ctgtcaagag	gatgcggcat	ctgtccacgg	600
gcacccatgac	tgggctggcc	atccagtatg	ccctgaacat	cgcattctca	gaagcagagg	660
gggcccggcc	cctgagggag	aatgtgccac	gggtcataat	gatcgtgaca	gatgggagac	720
ctcaggactc	cgtggccgag	gtggctgcta	aggcacggga	cacgggcatc	ctaactcttg	780
ccattggtgt	gggccaggta	gacttcaaca	ccttgaagtc	cattgggagt	gagcccatg	840
aggacatgt	cttccttggt	gccaatttca	gccagattga	gacgctgacc	tccgtgttcc	900
agaagaagtt	gtgcaaggcc	cacatgtgca	gcacctgga	gcataactgt	gccacttct	960
gcatcaacat	ccctggctca	tacgtctgca	ggtgcaaaaa	aggctacatt	ctcaactcgg	1020
atcagacgac	ttgcagaatc	caggatctgt	gtgccatgga	ggaccacaac	tgtgagcagc	1080
tctgtgtgaa	tgtgccgggc	tccttcgtct	gccagtgtca	cagtggctac	gccctggctg	1140
aggatgggaa	gaggtgtgtg	gctgtggact	actgtgcctc	agaaaaccac	ggatgtgaac	1200
atgagtgtgt	aaatgctgat	ggctcctacc	tttgccagtg	ccatgaagga	tttgctctta	1260
accagatga	aaaaacgtgc	acaaggatca	actactgtgc	actgaacaaa	ccgggctgtg	1320
agcatgagt	cgtcaacatg	gaggagagct	actactgccg	ctgccaccgt	ggctacactc	1380
tggaccccaa	tggcaaaaacc	tgcagccgag	tggaccactg	tgcacagcag	gaccatggct	1440
gtgagcagct	gtgtctgaac	acggaggatt	ccttcgtctg	ccagtgtctc	gaaggcttcc	1500
tcatcaacga	ggacctcaag	acctgctccc	gggtggatta	ctgcctgctg	agtgaccatg	1560
gttgtgaata	ctcctgtgtc	aacatggaca	gatacctttg	ctgtcagttg	cctgaggggac	1620
acgtgtctcc	cagcgatggg	aagacgtgtg	caaaatttga	ctcttgtgct	ctggggggacc	1680
acggttgtga	acattcgtgt	gtaagcagtg	aagattcgtt	tgtgtgccag	tgctttgaag	1740
gttatatact	ccgtgaagat	ggaaaaacct	gcagaaggaa	agatgtctgc	caagctatag	1800
accatggctg	tgaacacatt	tgtgtgaaca	gtgacgactc	atacacgtgc	gagtgtctgg	1860
agggattccg	gctcgtgag	gatgggaaac	gctgccgaag	gaaggatgtc	tgcaaatcaa	1920
cccaccatgg	ctgcgaacac	atttgtgtta	ataatgggaa	ttcctacatc	tgcaaatgct	1980
cagagggatt	tgttctagct	gaggacggaa	gacggtgcaa	gaaatgcact	gaaggcccaa	2040
ttgacctggt	ctttgtgatc	gatggatcca	agagtcttgg	agaagagaat	tttgaggctg	2100
tgaagcagtt	tgtcactgga	attatagatt	ccttgacaat	ttcccccaaa	gccgctcgag	2160
tggggctgct	ccagtattcc	acacagggtc	acacagagtt	cactctgaga	aacttcaact	2220
cagccaaaga	catgaaaaaa	gccgtggccc	acatgaaata	catgggaaag	ggctctatga	2280
ctgggctggc	cctgaaacac	atgtttgaga	gaagttttac	ccaaggagaa	ggggccaggc	2340
ccctttccac	aagggtgccc	agagcagcca	ttgtgttcac	cgacggacgg	gctcaggatg	2400
acgtctccga	gtgggccagt	aaagccaagg	ccaatgggat	cactatgtat	gctgttgggg	2460
taggaaaagc	cattgaggag	gaactacaag	agattgcctc	tgagcccaca	aacaagcatc	2520
tcttctatgc	cgaagacttc	agcacaatgg	atgagataag	tgaaaaactc	aagaaaggca	2580
tctgtgaagc	tctagaagac	tccgatggaa	gacaggactc	tccagcaggg	gaactgccaa	2640
aaacggtcca	acagccaaca	gaatctgagc	cagtcacccat	aaatatccaa	gacctacttt	2700
cctgttctaa	ttttgcagtg	caacacagat	atctgtttga	agaagacaat	cttttacggg	2760
ctacacaaaa	gctttcccat	tcaacaaaac	cttcaggaag	ccctttggaa	gaaaaacacg	2820
atcaatgcaa	atgtgaaaac	cttataatgt	tccagaacct	tgcaaacgaa	gaagtaagaa	2880
aattaacaca	gcgcttagaa	gaaatgacac	agagaatgga	agccctggaa	aatcgccctga	2940
gatacagatg	aagattagaa	atcgcgacac	atttgtagtc	attgtatcac	ggattacaat	3000
gaacgcagtg	cagagcccca	aagctcaggc	tattgttaaa	tcaataatgt	tgtgaagtaa	3060
aacaatcagt	actgagaaac	ctggtttgcc	acagaacaaa	gacaagaagt	atacactaac	3120
ttgtataaat	ttatctagga	aaaaaatcct	tcagaattct	aagatgaatt	taccaggtga	3180
gaatgaataa	gctatgcaag	gtattttgta	atatactgtg	gacacaactt	gcttctgcct	3240
catcctgcct	tagtgtgcaa	tctcatttga	ctatacgata	aagtttgcac	agtcttactt	3300



```

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatatat 3360
gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420
ttatacaata ttaaaattca ccacttcag                                     3449

```

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

```

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
  1                      5                      10                      15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
                      20                      25                      30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
                      35                      40                      45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
                      50                      55                      60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
                      65                      70                      75                      80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
                      85                      90                      95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
                      100                     105                     110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
                      115                     120                     125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
                      130                     135                     140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145                      150                      155                      160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
                      165                      170                      175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
                      180                      185                      190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
                      195                      200                      205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
210                      215                      220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

```

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn Val	Pro Gly Ser Phe	Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala Glu Asp	Gly Lys Arg Cys	Val Ala			
305	310	315	320			
Val Asp Tyr Cys	Ala Ser Glu Asn His	Gly Cys Glu His	Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys Gln Cys	His Glu Gly Phe	Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr Arg Ile	Asn Tyr Cys Ala	Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys Val Asn Met	Glu Glu Ser Tyr Tyr				
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr Leu Asp	Pro Asn Gly Lys Thr Cys				
385	390	395	400			
Ser Arg Val Asp	His Cys Ala Gln Gln Asp	His Gly Cys Glu Gln Leu				
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe Val Cys	Gln Cys Ser Glu Gly Phe				
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr Cys Ser	Arg Val Asp Tyr Cys Leu				
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr Ser Cys	Val Asn Met Asp Arg Ser				
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly His Val	Leu Arg Ser Asp Gly Lys				
465	470	475	480			
Thr Cys Ala Lys	Leu Asp Ser Cys Ala Leu	Gly Asp His Gly Cys Glu				
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp Ser Phe	Val Cys Gln Cys Phe Glu				
	500	505	510			

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
                             805                            810                            815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
                             820                            825                            830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
                             835                            840                            845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
                             850                            855                            860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
                             865                            870                            875                            880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
                             885                            890                            895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
                             900                            905                            910

Arg Tyr Arg  
                             915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                             oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                             oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagc gatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

```

ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt cgcgcagcct 60
cggcacctgc aggtccgtgc gtcccgcggc tggcgccccct gactccgtcc cggccagggg 120
gggccatgat ttccctcccc gggccccctgg tgaccaactt gctgcggttt ttgttcctgg 180
ggctgagtgc cctcgcgccc cctcgcggg cccagctgca actgcacttg ccgccaacc 240
ggttgcaggc ggtggagggg ggggaagtgg tgcttcagc gtggtacacc ttgcacgggg 300
aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaa 360
aaaaggagga tcaggtgttg tctacatca atggggtcac aacaagcaaa cctggagtat 420
ccttgggtcta ctccatgcc tcccggaacc tgtccctgcg gctggagggt ctccaggaga 480
aagactctgg cccctacagc tgcctcgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccctcctgcc 600
gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag tctccaagga 660
gtaagcccg tgtccaatac cagtgggatc ggcagcttcc atccttcag actttctttg 720
caccagcatt agatgtcatc cgtgggtctt taagcctcac caacctttcg tcttccatgg 780
ctggagtcta tgtctgcaag gccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
tggaagttag cacagggcct ggagctgcag tggttgctgg agctgttgtg ggtaccttg 900
ttggactggg gttgctggct gggtgggtcc tcttgtagca ccgcccgggc aaggccctgg 960
aggagccagc caatgatata aaggaggatg ccattgctcc ccggaccctg cctggccca 1020
agagctcaga cacaatctcc aagaatggga ccctttcctc tgtcacctcc gcacgagccc 1080
tccggccacc ccatggccct ccaggcctg gtgcattgac cccacgccc agtctctcca 1140
gccaggccct gccctcacca agactgcccc cgacagatgg ggcccacct caaccaatat 1200
cccccatccc tgggtggggt tcttcctctg gcttgagccg catgggtgct gtgcctgtga 1260
tgggtgctgc ccagagtcaa gctggctctc tggatatgat accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tctataagg gtcaccteta gcacagaggc ctgagtcag 1380
ggaaagagtc aactcctga ccttagtac tctgccccca cctctcttta ctgtgggaaa 1440
accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
attgggagga gcctccaccc acccctgact cctccttatg aagccagctg ctgaaattag 1560
ctactacca agagtgaggg gcagagactt ccagtcactg agtctcccag gccccttga 1620
tctgtacccc acccctatct aacacacccc ttggctccca ctccagctcc ctgtattgat 1680
ataacctgtc aggttggttt ggttaggttt tactggggca gaggataggg aatctcttat 1740
taaaactaac atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800
tttgatatgaa aaa 1813

```

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
 ggccacagca tcaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 43  
 gtgtgacaca gcgtgggc 18

<210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 44  
 gaccggcagg cttctgcg 18

<210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 45  
 cagcagcttc agccaccagg agtgg 25

<210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 46  
 ctgagccgtg ggctgcagtc tcgc 24

<210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 cgccaccact gcggccaccg ccaatgaaac gcctcccgt cctagtgggt tttccactt 60  
 tgttgaattg ttctataact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120  
 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcc tttagataat gtctgtatag ctgcaaata taataaaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
 taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600  
 aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660  
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720  
 cttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780  
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840  
 atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900  
 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960  
 acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttcagtaat ttcagtctca atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080  
 taacatttac attaatgcat cgaaagggtc cagataggta taggagtcta tgtgcatttt 1140  
 ggaattactc acctgatacc atgaatggca gctggctctc agagggctgt gagctgacat 1200  
 actcaaatga gaccacaccc tcatgccgt gtaatcacct gacacatttt gcaattttga 1260  
 tgtcctctgg tccttcattt ggtattaaag attataatat tcttacaagg atcactcaac 1320  
 taggaataat tatttcactg atttgccttg ccatatgcat ttttaccttc tgggtcttca 1380  
 gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440  
 ctgaacttgt ttttcttggt gggatcaata caaatactaa taagctcttc tgttcaatca 1500  
 ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560  
 tacatctcta tctcattgtt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620  
 tttatatctt tggctatcta agcccagccg tggtagttgg attttcggca gcactaggat 1680  
 acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaacaac tttatttgga 1740  
 gttttatagg accagcatgc ctaatcattc ttgttaatct cttggccttt ggagtcacat 1800  
 tatacaaagt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860  
 taaggtcttg tgcaagagga gccctcgtc ttctgttctt tctcggcacc acctggtact 1920  
 ttggggttct ccattgtgtg cagcactcag tgggtacagc ttacctcttc acagtcagca 1980  
 atgctttcca ggggatgttc atttttttat ttctgtgtgt tttatctaga aagattcaag 2040  
 aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100  
 agagaatggt ggataattac aactgcacaa aaataaaaaat tccaagctgt ggatgaccaa 2160

```

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtattttaa 2220
atcagttttt ctgtttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatatatt 2340
ggaaagtaat tggttttctca ggagtgatat cactgcaccc aaggaaagat tttctttcta 2400
acacgagaag tatatgaatg tcttgaagga aaccactggc ttgatatttc tgtgactcgt 2460
gttgcccttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
cataagagaa tgaaggggca gaatatcaaa cagtgaaaag ggaatgataa gatgtatttt 2580
gaatgaactg ttttttctgt agactagctg agaaattgtt gacataaaat aaagaattga 2640
agaaacacat tttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700
agacttctgt ttgctaaatc tgtttctttt tctaatatcc taaaaaaaaa aaaaagggtt 2760
acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa

```

```

<210> 49
<211> 690
<212> PRT
<213> Homo sapiens

```

```

<400> 49
Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
 1             5             10             15

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20             25             30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35             40             45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50             55             60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65             70             75             80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85             90             95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100            105            110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115            120            125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130            135            140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145            150            155            160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165            170            175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

			180				185				190				
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val
		195				200						205			
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys
		210				215				220					
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe
225					230				235						
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys
				245				250				255			
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met
		260						265				270			
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala
		275				280						285			
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser
290						295				300					
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln
305				310						315		320			
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile
				325				330				335			
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys
		340						345				350			
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser
		355				360						365			
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp
370						375				380					
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser
385				390						395		400			
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly
				405				410				415			
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln
		420						425				430			
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr
		435				440				445					
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys
450						455				460					

```

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465                               470                               475                               480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
                               485                               490                               495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
                               500                               505                               510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
                               515                               520                               525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
                               530                               535                               540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545                               550                               555                               560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
                               565                               570                               575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
                               580                               585                               590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
                               595                               600                               605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610                               615                               620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625                               630                               635                               640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
                               645                               650                               655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
                               660                               665                               670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675                               680                               685

Leu Arg
690

```

&lt;210&gt; 50

&lt;211&gt; 589

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (61)

<223> a, t, c or g

<400> 50

```

tggaaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaatggca atgttgcagt tgcattttta tattataaga 120
gtattgggcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacg aaaggtcaca 300
gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tgggtcttcag agggctgtga gctgacatac tcaaatgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta ttctactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggccctcctcc tcccgcagat ccgaacgggc tgggcggggg cccccggct 120

```

gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240
tgctcgggtg tcttgggcac ctaccctggg ggcccgttaag gcgctactat ataaggctgc 300
cggcccggag ccgccgcgcc gtcagagcag gagcgctgcg tccaggatct agggccacga 360
ccatcccaac ccggcactca cagccccgca gcgcaccccg gtccgcgccc agcctcccgc 420
acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540
cttctcggac gcggggcccc acgtgcaacta cggctggggc gaccccatcc gcctgcggca 600
cctgtacacc tccggccccc acgggctctc cagctgcttc ctgcgcaccc gtgccgacgg 660
cgtcgtggac tgcgcgcggg gccagagcgc gcacagtttg ctggagatca aggcagtgc 720
tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgccga 780
cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840
ccgccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900
cagtgcctaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatcttct 960
gcccattgctg cccatggtcc cagaggagcc tgaggacctc agggggccact tggaaatctga 1020
catgtttctct tcgcccctgg agaccgacag catggacceca tttgggcttg tcaccggact 1080
ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140
tgctgccagg ggctgtggtg cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200
agtccacgtt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260
tccattggca gtgccagttt ctagccaata gacttgctcg atcataacat tgtaagcctg 1320
tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380
gctgcactgt ctcagttctg cttgaatacc tccatcgatg gggaactcac ttcctttgga 1440
aaaattctta tgtcaagctg aaattctcta attttttctc atcacttccc caggagcagc 1500
cagaagacag gcagtagttt taatttcagg aacaggatgat ccactctgta aaacagcagg 1560
taaatttcac tcaaccccat gtgggaattg atctatatct ctacttcag ggaccatttg 1620
cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa tccccctga 1740
ggccagttct gtcattggatg ctgtcctgag aataacttgc tgtcccgggtg tcacctgctt 1800
ccatctccca gccaccagc cctctgccca cctcacatgc ctccccatgg attggggcct 1860
cccaggcccc ccacettatg tcaacctgca cttcttgttc aaaaatcagg aaaagaaaag 1920
atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacct 1980
gaacccttcc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100
gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

```

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1                      5                      10                      15

```

```

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
                20                25                30

```

```

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
    35                40                45

```

```

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
    50                55                60

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

gcctcccgtg ctccctgagc agtgccaaac agcggcagtg ta

42



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggcgccctt gggctatcat aaggcctatg gggtttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatct tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggagg aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgatttttaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatata gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccgca attctgttgg atatcgagg tgcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ctttagtgat 840  
 ttccgtttgt ggccttgggt tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctccctccag aagagtaatt ctcatctaa agccacgaca atgagtgaat atgtgcagt 960  
 gctcacgcct gtaatcccag cactttggaa ggcgcggcgg ggcggatcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggagggttc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact gggttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
 35 40 45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
 50 55 60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
 65 70 75 80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
 85 90 95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
 100 105 110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
 115 120 125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
 130 135 140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
 145 150 155 160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
 165 170 175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
 180 185 190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
 195 200 205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
 210 215 220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
 225 230 235 240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
 245 250 255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
 260 265 270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
 275 280 285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
 290 295 300  
 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

&lt;210&gt; 65

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 65

atcgttgtga agttagtgcc cc

22

&lt;210&gt; 66

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 66

acctgcgata tccaacagaa ttg

23

&lt;210&gt; 67

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

&lt;210&gt; 68

&lt;211&gt; 2639

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaag 60  
agaaagaaga ggaagatgtt gggcaacatt tatttaacat gtcacacgc ccggaccctg 120  
gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
aaataaatga attactcaat ctccatagac catctataca tactccacct tcaaaaagta 240  
catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300  
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360  
tggcattcat catttgacaa atgcaagcat cttccttata aatcagctcc tattgaactt 420  
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtag 540

```

aagctgtaga taaaaaagtg gattgtccac gggtatgtac gtgtgaaatc aggccttggt 600
ttacacccag atccatttat atggaagcat ctacagtgga ttgtaatgat ttaggtcttt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcttttctg 840
tgtacctaga ggaaaaacaaa cttactgaac tgccctgaaaa atgtctgtcc gaactgagca 900
acttacaaga actctatatt aatcacaaact tgctttctac aatttcacct ggagccttta 960
ttggcctaca taatcttctt cgacttcac tcaattcaaa tagattgcag atgatcaaca 1020
gtaagtgggt tgatgctctt ccaaactctag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac ttttaagcctc ttatcaatct tgcgagcctg gttatagctg 1140
gtataaacct cacagaaata ccagataacg ccttggttg actggaaaac ttagaaaagca 1200
tctcttttta cgataacagg cttattaaag taccctcatgt tgctcttcaa aaagttgtaa 1260
atctcaaatt tttggatcta aataaaaaatc ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacccta 1440
gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcactcatgc 1500
tgaacagcaa tgctctcagt gccctgtacc atgggtaccat tgagtctctg ccaaacccta 1560
aggaaatcag catacacagt aaccccatca ggtgtgactg tgtcatccgt tggatgaaca 1620
tgaacaaaac caacattoga ttcattggagc cagattcact gttttgcgtg gaccacactg 1680
aattccaagg tcagaatggt cggaagtgc atttcaggga catgatggaa atttgtctcc 1740
ctcttatagc tctgagagc tttccttcta atctaaatgt agaagctggg agctatgttt 1800
cctttcactg tagagctact gcagaaccac agcctgaaat ctactggata acaccttctg 1860
gtcaaaaact cttgcctaata accctgacag acaagttcta tgtccattct gagggaaacac 1920
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgtata gcaactaacc 1980
tagttggcgc tgacttgaag tctgttatga tcaaagtggg tggatctttt ccacaagata 2040
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100
ggaaagcaag ttctaaaatt ctcaaactta gtgttaaata gacagccttt gtcaagactg 2160
aaaattctca tgctgcgcaa agtgctcgaa taccatctga tgtcaaggta tataatctta 2220
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280
aaaacagaaa aaaatgtgta aatgtcacca ccaaagggtt gcacctgat caaaaagagt 2340
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400
gtgtgatatg tcttatcagc tgccctctctc cagaaatgaa ctgtgatggt ggacacagct 2460
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520
taaactctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggtttacc aacaaatatg tcttaaaaac caccaaggaa acctactcca aaaatgaac 2639

```

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

```

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
  1                      5                      10                      15

```

```

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
                20                      25                      30

```

```

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
    35                      40                      45

```

```

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
    50                      55                      60

```

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

	340		345		350										
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
	355						360					365			
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
	370					375					380				
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
385					390					395					400
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
			420					425						430	
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
	435						440					445			
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
	450					455						460			
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
465					470					475					480
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
				485					490					495	
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
			500					505						510	
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
	515						520						525		
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
	530					535						540			
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
545					550					555					560
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565					570					575	
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys
			580					585					590		
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn
	595						600						605		
Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn
	610					615					620				

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

```

gcccgggact ggcgcaaggt gcccaagcaa ggaaagaaat aatgaagaga cacatgtggt 60
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120
ttaccacgct tggttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taaccctgtc cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300
ttcctctggg ggttttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360
tcttctctct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420
tgaaatTTTT aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540
cgacaatcgg attcaaagtg tgcacaaaaa tgcttcaat aacctgaagg ccagggccag 600
aattgccaac aacctctggc actgcgactg tactctacag caagttctga ggagcatggc 660
gtccaatcat gagacagccc acaactgat ctgtaaaacg tccgtgttgg atgaacatgc 720
tggcagacca ttctcaatg ctgccaacga cgtgacctt tgtaacctcc ctaaaaaaac 780
taccgattat gccatgctgg tcaccatggt tggctgggtc actatgggtg tctcatatgt 840
ggtatattat gtgaggcaaa atcaggagga tgcccgaga cacctcgaat acttgaaatc 900
cctgccaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080
tatgccactg ctgaactttt acaaaacact acaacataaa taatttgagt ttaggtgatc 1140
caccctttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcactattta ataatgaaat ttattttttt aatttaaaag caaataaaaag 1260
cttaactttg aacctggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

```

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

accgagccga gcggaccgaa ggcgcgcgcg agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtgag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctctgctgg 120
tgctgggctc agtgctgtca ggctcggcca cgggctgccc gcccgcctgc gactgctccg 180
cccaggaccg cgctgtgctg tgcacccgca agtgctttgt ggcagtcccc gagggcatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tgagagccgg cgcttcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctactgg actacatggt tcaggacctg tacaacctca 540
agtcaactgga gggtggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgctc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctcttcaag aggtgtgacc gactcaaggt cttggagatc tcccactggc 780
cctacttgga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggcctg ccgccaccta gtctatctcc 900
gcttcctcaa cctctctac aacccccatc gcaccattga gggctccatg ttgcatgagc 960
tgctccgggt gcaggagatc cagctgggtg gcgggcagct ggcggtgggt gagccctatg 1020
ccttccgcgg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tgagggaatc agtcttccac tcgggtgggca acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgactgtcgg ctctgtggg tgttccggcg ccgctggcgg ctcaacttca 1200
accggcagca gcccacgtgc gccacgccc agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgccc aactacttca cctgcgcgcg cggccgcac cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacggtgca gtttgtgtgc cgggccgatg 1380
gcgaccgcgc gcccgccatc ctctggctct caccgcgaaa gcacctggtc tcagccaaga 1440
gcaatgggcg gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gccagggtac 1500
aggacaacgg cacgtacctg tgcctgcggg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgcccc actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag aggcccaacag caccgcgcgc actgtgcctt 1680
tccccttcga catcaagacc ctcatcatcg ccaccacat gggcttcac tctttcctgg 1740
gcgtcgtcct cttctgctcg gtgctgctgt ttctctggag ccggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggcatc agctccgccc 1860
acgcgccccg caagtccaac atgaagatga tataggccg gggcgggggg cagggacccc 1920
cggcgggccg ggcaggggaa ggggcctggg cgccacctgc tcaacttcca gtccctccca 1980
cctcctccct accttctac aacgcttctc tttctccctc ccgcctccgt cccctgctgc 2040
ccccgcgcag cctcaccac ctgccctcct totaccagga cctcagaagc ccagacctgg 2100
ggacccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaa 2290

```

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
1           5           10           15

```

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30  
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590	
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser			
595	600	605	
Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile			
610	615	620	
<210> 74			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 74			
tcacctggag cctttattgg cc			22
<210> 75			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 75			
ataccagcta taaccaggct gcg			23
<210> 76			
<211> 52			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 76			
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg			50
gg			52
<210> 77			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			

<400> 77  
 ccatgtgtct cctcctacaa ag 22  
  
 <210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 78  
 gggaatagat gtgatctgat tgg 23  
  
 <210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 79  
 cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50  
  
 <210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 80  
 agcaaccgcc tgaagctcat cc 22  
  
 <210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 81  
 aaggcgcggt gaaagatgta gacg 24  
  
 <210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cggggggcgc ctttcgggtca 60  
 acatcgtagt ccacccccctc cccatcccca gcccccgggg attcaggctc gccagcgccc 120  
 agccagggag ccggccggga agcgcgatgg gggccccagc cgcctcgtc ctgctcctgc 180  
 tcctgctgtt cgctgctgc tgggcgccc ggggggcaa cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctgggtggcac cgtgggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaacc tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtag acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaagt cctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggt gaccaagaac 660  
 tccacggaga accaaccgac atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gtcgggtgac attccagggt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttataca 840  
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgaggggcag aagctggtgc 900  
 tacactgtga gggtcgcggc aatccagtc cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgcctgat ctccctttc ctcaacaaga 1020  
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgtaaatgac ccagtcagg tgcctcctc ctccagcacc taccacgcca 1140  
 tcatcggtgg gatcgtggct ttcatgtct tctgctgct catcatgctc atcttctctg 1200  
 gccactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgtccaga cgcggacacg gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320  
 acaagaagga atatttcac tagaggcgcc tgcccacttc ctgcgcccc caggggccct 1380  
 gtggggactg ctggggccgt caccaaccgg gacttgtaga gagcaaccgc agggccgccc 1440  
 ctcccgcttg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggt 1500  
 tttgtactcg gtttggaatg gggaggagg agggcggggg gaggggaggg ttgccctcag 1560  
 ccctttccgt ggcttctctg catttgggtt attattattt ttgtaacaat cccaaatcaa 1620  
 atctgtctcc aggttgaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

&lt;400&gt; 87

cctagcacag tgacgaggga cttggc

26

&lt;210&gt; 88

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc

50

&lt;210&gt; 89

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt

50

&lt;210&gt; 90

&lt;211&gt; 2755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

```

gggggttagg gaggaaggaa tccaccccca cccccccaaa ccccttttctt ctccctttcct 60
ggcttcggac attggagcac taaatgaact tgaatttgtgt ctgtggcgag caggatgggc 120
gctgttactt tgtgatgaga tcggggatga attgtctgct ttaaaaatgc tgctttggat 180
tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240
agagaagatc tgttcctgca atgagataga aggggacctc cacgtagact gtgaaaaaaaa 300
gggcttcaca agtctgcagc gtttcactgc cccgacttcc cagttttacc atttatttct 360
gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggg 420
tagtttgac atggaaaaca atggcttgca tgaaatcggt ccggggggtt ttctggggct 480
gcagctggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540
ttttctgggg ctggacgac tggaatatct ccaggtgat ttttaatttat tacgagatat 600
agaccggggg gccttcagg acttgaacaa gctggagggtg ctcattttaa atgacaatct 660
catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tcgacctccg 720
gggtaacagg ctgaaaacgc tgccctatga ggagggtcttg gagcaaatcc ctggtattgc 780
ggagatcctg ctagaggata acccttgga ctgcacctgt gatctgctct ccctgaaaga 840
atggctggaa aacattccca agaatgccct gatcggccga gtggtctgctg aagcccccac 900
cagatgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960
ccgagtggat tctagtctcc cggcgcctcc tgcccaagaa gagacctttg ctctgggacc 1020
cctgccaaact cctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

```

```

aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140
agcgacgggt agctccagga acaaaccctt agctaacagt ttaccctgcc ctgggggctg 1200
cagctgcgac cacatcccag ggtcgggttt aaagatgaac tgcaacaaca ggaacgtgag 1260
cagcttggct gatttgaagc ccaagctctc taacgtgcag gagcttttcc tacgagataa 1320
caagatccac agcatccgaa aatcgcaact tgtggattac aagaacctca ttctgttgga 1380
tctgggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttggacct 1440
caggtggcta tacatggata gcaattacct ggacacgtg tcccgggaga aattcgcggg 1500
gctgcaaaac cttagagtacc tgaacgtgga gtacaacgt atccagctca tcctcccggg 1560
cactttcaat gccatgcccc aactgaggat cctcattctc aacaacaacc tgctgaggtc 1620
cctgcctgtg gacgtgttcg ctgggggtctc gctctctaaa ctgagcctgc acaacaatta 1680
cttcatgtac ctcccggtgg caggggtgct ggaccagtta acctccatca tccagataga 1740
cctccacgga aacccctggg agtgcctctg cacaattgtg cctttcaagc agtgggcaga 1800
acgcttgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgccg tgaacttctt 1860
tagaaaggat ttcattgctc tctccaatga cgagatctgc cctcagctgt acgctaggat 1920
ctcgcccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga ccgggacgca 1980
ctccaactcc tacctagaca ccagcagggt gtccatctcg gtgttggtcc cgggactgct 2040
gctggtgttt gtcacctccg ccttcaccgt ggtgggcatg ctctgttcta tcctgaggaa 2100
ccgaaagcgg tccaagagac gagatgccaa ctctcccgcg tccgagatta attccctaca 2160
gacagtctgt gactcttctt actggcacia tgggccttac aacgcagatg gggcccacag 2220
agtgtatgac tgtggctctc actcgctctc agactaagac cccaaccca ataggggagg 2280
gcagagggaa ggcgatacat ccttccccac cgcaggcacc ccgggggctg gagggcgctg 2340
taccocaaatc cccgcgccat cagcctggat gggcataagt agataaataa ctgtgagctc 2400
gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
tgagagagct ggagagcgca gccagctcgc tctttgctga gagcccttt tgacagaaag 2520
cccagcacga ccctgctgga agaactgaca gtgcctcgc cctcgcccc ggggcctgtg 2580
gggttgatg ccgcggttct atacatata acatataatc acatctatat agagagatag 2640
atatctattt tccccctgtg gattagcccc gtgatggctc cctgttggct acgcagggat 2700
gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755

```

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

```

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1                      5                      10                      15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
          20                      25                      30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
          35                      40                      45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
          50                      55                      60

```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
          65                      70                      75                      80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
          85                      90                      95

```

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 92  
gttggatctg ggcaacaata ac 22

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 93  
attgttgtgc aggctgagtt taag 24

<210> 94  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 94  
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<400> 95  
agtcgactgc gtccctgtga cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60  
gctgcaccgg gcctggcagc gctccgcaca catttctgt cgcggcctaa gggaaactgt 120  
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

```

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaatgaggc cggcgttcgc cctgtgcctc ctctggcagg cgtctgggcc 360
cgggccgggc ggccggcgaac accccactgc cgaccgtgct ggctgctcgg cctcgggggc 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcacctc 480
gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540
cctcggggca ggcccagggc ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600
ggagcgcagg cgttcccact gcaccctgga gaacgagcct ttgcgggggt tctcctggct 660
gtcctccgac cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720
ctcctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggctc agcccgcagg 780
ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840
ggtcttgtgt cctgcgcgcg gccccggggc cgctctaac ttgagctatc gcgcgcctt 900
ccagctgcac agcgcgcgctc tggacttcag tcacactggg accgaggtga gtgcgctctg 960
ccggggacag ctcccgatct cagttacttg catcgcgagc gaaatcggcg ctgcgtggga 1020
caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctccgtg ctggcaaatg 1080
cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140
cttcgagctg ggggaaggac gccgctcttg tgtgaccagt ggggaaggac agccgacct 1200
tggggggacc ggggtgcca ccaggcgcgc gccggccact gcaaccagcc cgtgcgcga 1260
gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320
agacaattca gtaacatcta ttcctgagat tcctcgatgg ggatcacaga gcacgatgtc 1380
tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccccat cagggagcgt 1440
gatttccaag tttaattcta cgacttcctc tgccactcct caggctttcg actcctcctc 1500
tgccgtggtc ttcataattg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560
agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttcccagc caaggaagga 1620
gtctatgggc ccgcggggc tggagagtga tcctgagccc gctgctttgg gctccagttc 1680
tgcacattgc acaaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740
gggtgccttg ctggcggagt cccctcttgg ctctagtgat gcatagggaa acaggggaca 1800
tgggcactcc tgtgaacagt ttttacttt tgatgaaacg gggaaccaag aggaacttac 1860
ttgtgtaact gacaatttct gcagaaatcc cccttcctc aaattccctt tactccactg 1920
aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980
aggatggtga tactggggga ccgggtagtg ctggggagag atattttctt atgtttattc 2040
ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctacaaa atggaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220
gttgat

```

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

```

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
  1                      5                      10                     15

```

```

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
                20                      25                     30

```

```

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
    35                      40                     45

```

```

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
    50                      55                     60

```

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgatgccca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20



<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 99  
 acagagcaga gggcgccttg 20  
  
 <210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 100  
 tcagggacaa gtggtgtctc tccc 24  
  
 <210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 101  
 tcagggaagg agtgtgcagt tctg 24  
  
 <210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 102  
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50  
  
 <210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

```

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatccccggg ctacctgggc cgccccgcgg cgggtgcgcg gtgagaggga gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtgtgt gccagtgtga gcggcgggtg gagcgcggtg 240
ggtgcggagg ggcgtgtgtg ccggcgcgcg cgccgtgggg tgcaaaccac gagcgtctac 300
gctgccatga ggggcgcgaa cgccctgggc ccactctgcc tgctgtctgg tgcgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gattttattg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tccgaagga aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaac cagctggcaa tggcttcagt 720
gccatgttct ccgctgctga accaaacgaa agaggggagc agtattgtgg aggactcctt 780
gacagacctt ccgctctttt taaaaccccc aactggccag accgggatta cctgcagga 840
gtcacttgtg tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cगतatgatt atgtggctgt gtttaattggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtc accctgcgcca 1020
attgtgtctg agagaaatga acttcttatt cagtttttat cagacttaag ttttaactgca 1080
gatgggttta ttggtcacta catattcagg ccaaaaaaac tgcctacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg tcgtctgcaa gcagtgccct ctctcagaa gaggtctaaa ttacattatt 1440
atgggccaag taggtgaaga tgggcgaggg aaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca ttttaagctgt attctgccat tgcccttgaa agatctatgt tctctcagta 1620
gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactcttc acatgatgga ggtatgaggc ctccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttgga gcgtttattt atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1                      5                      10                      15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
                20                      25                      30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
                35                      40                      45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
                50                      55                      60

```

Val 65	Pro	Glu	Gly	Lys	Val 70	Val	Val	Leu	Asn	Phe	Arg	Phe	Ile	Asp	Leu 80
Glu	Ser	Asp	Asn	Leu 85	Cys	Arg	Tyr	Asp	Phe 90	Val	Asp	Val	Tyr	Asn 95	Gly
His	Ala	Asn	Gly 100	Gln	Arg	Ile	Gly	Arg 105	Phe	Cys	Gly	Thr	Phe 110	Arg	Pro
Gly	Ala	Leu 115	Val	Ser	Ser	Gly	Asn 120	Lys	Met	Met	Val	Gln 125	Met	Ile	Ser
Asp	Ala 130	Asn	Thr	Ala	Gly	Asn 135	Gly	Phe	Met	Ala	Met 140	Phe	Ser	Ala	Ala
Glu 145	Pro	Asn	Glu	Arg	Gly 150	Asp	Gln	Tyr	Cys	Gly 155	Gly	Leu	Leu	Asp	Arg 160
Pro	Ser	Gly	Ser	Phe 165	Lys	Thr	Pro	Asn 170	Trp	Pro	Asp	Arg	Asp 175	Tyr	Pro
Ala	Gly	Val	Thr 180	Cys	Val	Trp	His	Ile 185	Val	Ala	Pro	Lys	Asn 190	Gln	Leu
Ile	Glu	Leu 195	Lys	Phe	Glu	Lys	Phe 200	Asp	Val	Glu	Arg	Asp 205	Asn	Tyr	Cys
Arg 210	Tyr	Asp	Tyr	Val	Ala	Val 215	Phe	Asn	Gly	Gly	Glu 220	Val	Asn	Asp	Ala
Arg 225	Arg	Ile	Gly	Lys	Tyr 230	Cys	Gly	Asp	Ser	Pro 235	Pro	Ala	Pro	Ile	Val 240
Ser	Glu	Arg	Asn 245	Glu	Leu	Leu	Ile	Gln 250	Phe	Leu	Ser	Asp	Leu 255	Ser	Leu
Thr	Ala	Asp	Gly 260	Phe	Ile	Gly	His	Tyr 265	Ile	Phe	Arg	Pro	Lys 270	Lys	Leu
Pro	Thr	Thr	Thr 275	Glu	Gln	Pro	Val 280	Thr	Thr	Thr	Phe 285	Pro	Val	Thr	Thr
Gly 290	Leu	Lys	Pro	Thr	Val	Ala 295	Leu	Cys	Gln	Gln	Lys 300	Cys	Arg	Arg	Thr
Gly 305	Thr	Leu	Glu	Gly	Asn 310	Tyr	Cys	Ser	Ser	Asp 315	Phe	Val	Leu	Ala	Gly 320
Thr	Val	Ile	Thr 325	Thr	Ile	Thr	Arg	Asp	Gly 330	Ser	Leu	His	Ala 335	Thr	Val
Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala

	340		345		350										
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro
	355						360				365				
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu
	370				375					380					
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys
385					390				395						400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys	
			405				410						415		

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

```

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccg cgggctgggg cggctcgcttc 60
ttccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct ccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgcctcagcc ccattcggtg 240
catacctgcc ggggactggt tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgcttgggag gaagagaatt tgtccaaata caaagacagt 360
gagaccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgcctgctgg agctgagtga ggagctggtg gagagctggt ggtttcacaa gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgaggc 540
accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cgggtggctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc ccctgtgccc gatgctcagg acctgaggaa 780
tcaaactgtt tgcaatgcaa gaagggtggt gccctgcac acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaaag gcctgcctag gctgcatggg ggcagggcca 960
ggtcgctgta agaagtgtag ccctggctat cagcagggtg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcatctgtgc cgagggtac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcaactggcca cgctggctgc taaggcgac 1260
ttggtgttca ccgccatctt cattggggct gtggcgcca tgactggcta ctggttgtca 1320
gagcgagtg accgtgtgct ggagggtctt atcaagggca gataatcgcg gccaccacct 1380
gtaggacctc ctcccaccca cgctgcccc agagcttggg ctgcccctct gctggacact 1440
caggacagct tggtttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500
gccagggtac ccaggccccg gcagacaagg cccctggggt aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttctt taatggtggc tgctagagct ttggcccctg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tctgttctg 1740
tgttcaccac atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1                      5                      10                      15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20                      25                      30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35                      40                      45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50                      55                      60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                          360                          365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
      370                          375                          380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                          390                          395                          400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                           405                          410                          415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tcctccaggg 60  
 cagcaccatg cagcccctgt ggctctgctg ggcactcttg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcatcccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagagggt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcatggagc agcggctgcc gcccaacagc gagctggtgc aggcctgct 420  
 gcggctcttc caggagccgg tccccaaagg cgcgctgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggctggt gtcggtccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggcctgga acttctggca gcagctgagc cggccccggc agccgctgct 660  
 gctacagggtg tcggtgcaga gggagcatct gggcccgcgt gcgtccggcg ccacaagct 720  
 ggtccgcttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gaggcctgg ccttcaagtg gccgtttctg gggcctcgac agtgcctgc 1020  
 ctcgagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccagggtggtc agcctgcccc acatgagggg gcagaagtgc agctgtgcct cggatggtgc 1140  
 gctcgtgcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgctct ctagtgagcc ctgaatttgc ttctctgac aagttacctc 1320  
 acctaatatt tgcttctcag gaatgagaat ctttgccac tggagagccc ttgctcagtt 1380  
 ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaaagcca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtcctcc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
                   340                  345                  350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
                   355                  360                  365

<210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 115  
 aggactgccca taacttgctt g 21

<210> 116  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 116  
 ataggagttg aagcagcgct gc 22

<210> 117  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
 <211> 1857  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcata tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgatg ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac cegtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcagtga agctgtggag cggaatgtgg gggatcatcg ggcagccgtc 780
cttghtaacc tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840
ggcacttttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtgcctgaa gtgaaggaga attcaaacag acctcgatc tcctgggtgtg agcctggctg 960
gctcacgcc tatcatctgc atttgcctta ctccaggtgt accggactct ggccccctgat 1020
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
tttcctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200
agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttgggtgat gacactggg 1440
tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500
ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttgtt gtggagagca tagtaaat ttagagaact tgaagccaaa aggatttaaa 1620
accgtgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcagggcga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaacc tactggaaat acaaagttag ccaggcatgg tgggtcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

```

```

<210> 119
<211> 299
<212> PRT
<213> Homo sapiens

```

```

<400> 119
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1             5             10             15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20             25             30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35             40             45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50             55             60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65             70             75             80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85             90             95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tggtgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctgggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 125

actcagcagtg ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

cagcgcgtgg cggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcaggttg 60  
gagcgtggcg aacagggggt ctgggcctgg cgtgctgct gctgctcggc ctgggactag 120  
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300  
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360  
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgtgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660  
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctccctcttt 780  
tgtcctggct ccgagcccag gagcgccctc gccactggg gttactggtg gccatgaagg 840  
agtcctctgt gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccttgagca ctccctatgg agatccgggg 1080  
agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                             85                            90                            95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                             100                            105                            110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                             115                            120                            125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                             130                            135                            140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                             145                            150                            155                            160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                             165                            170                            175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                             180                            185                            190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                             195                            200                            205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                             210                            215                            220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                             225                            230                            235                            240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                             245                            250                            255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                             260                            265                            270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                             275                            280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cgggtctcgtc cgctcgcgca gcggcgaggc cagagggtcgc gcacagatgc 60  
 gggtttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaacccga 180  
 gcaatggaga tggatttcta gaggcagcag agcagcagca gcaacctcag tccccccaga 240  
 gactcttggtc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300  
 cgggcggggtt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360  
 ggacccccag cggagggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatacg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600  
 atgaaggatt caagatccgg taccgccgac tacacaatat ggtttcatta tgcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaatggt ggtcacgga gatttcgtct gccacccgag gccttgtagc cgctacaacc 960  
 acggaactgt ggtggagttt tactgcatc ctggctacag cctcaccagc gactacaagt 1020  
 acatcacctg ccagtatgga gagggttttc cttcttatca agtctactgc atcaaatacg 1080  
 agcaaactgt gccagcacc catgagaccc tcttgaccac gtggaagatt gtggcggttca 1140



```

cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcggtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggctgc cccttaccg 1380
tggaacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
  1             5             10             15

```

```

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
      20             25             30

```

```

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
    35             40             45

```

```

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
    50             55             60

```

```

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
    65             70             75             80

```

```

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
      85             90             95

```

```

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
    100             105             110

```

```

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
    115             120             125

```

```

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
    130             135             140

```

```

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
    145             150             155             160

```

```

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
      165             170             175

```

```

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```

[illegible]

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133  
 atctcctatc gctgctttcc cgg 23

<210> 134  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc 23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct 50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgtccgcgc cctccccccc gctcccgctg cggtcgcgtc gtggcctaga 60  
 gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120  
 ccgtagegcc cgagtgtcgg ggggcgcacc cgagtcggggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240  
 tgagtgcctc ggatttgac ctacagaggag ggcagccagt ctgccgggga gggacacaga 300

```

ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgagggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaataatt 720
ctgatgagaa accagcagtt ctttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccctt ctccctctcc 900
ttgtgggtcac cacagttgta tggtgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacataataa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgttggt acccccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaaa                                     1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

&lt;210&gt; 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgagg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240  
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcagtc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcgttc 660  
 cactaacatt tttcggaatc tggagtccac ccgttggttg ctggctgggc ttttccagtg 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcctcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtagggccc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gacctggggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1             5             10             15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20             25             30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35             40             45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50             55             60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65             70             75             80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85             90             95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100            105            110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115            120            125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130            135            140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145            150            155            160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165            170            175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

```

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcacc caatcagtcg gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccacaga 480
gagctctttc tccccagtcg cagagggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccggggc gcaaaggtgg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgatg ggggctctgt 900
ctgtgatgac aactggggag aaaaggagga ccagggtgta tgcaagcaac tgggctgtgg 960
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020
ctggctggat aatgttcgtt gctcagggga ggagcagtcg ctggagcagt gccagcacag 1080
attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140
ggtgggcacg atctaactct ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200
atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260
acttataact ggtgcccctg attctcaggg cttcagagtt ggatcagaac ttacaacatc 1320
aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttctatgtc 1380
tccacattgc acacagcaga ttcacagcct ccataattgt gtgtatcaac tacttaaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgtttctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt gggttatggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

```

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
    115                      120                      125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
    130                      135                      140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
    145                      150                      155                      160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
    165                      170                      175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
    180                      185                      190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
    195                      200                      205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
    210                      215                      220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
    225                      230                      235                      240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
    245                      250                      255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
    260                      265                      270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
    275                      280                      285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
    290                      295                      300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
    305                      310                      315                      320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
    325                      330                      335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
    340                      345

```

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

```

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60
acccacgcgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120
gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
gaatgctgtg gtggtgatca caggcgccac ctgagggtg ggcaaagaat gtgcaaaagt 300
cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagt ccatcacgcg 840
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
cttactgcct tccttggctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1             5             10             15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
      20             25             30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35             40             45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50             55             60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65             70             75             80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
      85             90             95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100            105            110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115            120            125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130            135            140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145            150            155            160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
      165            170            175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180            185            190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195            200            205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

1140  
 1200  
 1260  
 1320  
 1380  
 1427  
 153  
 310  
 PRT  
 Homo sapiens  
 153  
 Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
 1 5 10 15  
 Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
 20 25 30  
 Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
 35 40 45  
 Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
 50 55 60  
 Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
 65 70 75 80  
 Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
 85 90 95  
 Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala  
 100 105 110  
 Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
 115 120 125  
 Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
 130 135 140  
 Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
 145 150 155 160  
 Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
 165 170 175  
 Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
 180 185 190  
 Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
 195 200 205  
 Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220	
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg			
225	230	235	240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu			
	245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val			
	260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu			
	275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu			
	290	295	300
Arg Lys Ser Lys Asn Ser			
305	310		
<210> 154			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 154			
ggtgctaaac tggtgctctg tggc			24
<210> 155			
<211> 20			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 155			
cagggcaaga tgagcattcc			20
<210> 156			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			

<400> 156  
tcatactgtt ccattctcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctggtggt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggaactgg gtgccaaggt 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatatt agtaaataat gctgggtgtag tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagtgt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagtct 1140  
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260  
taatttccaa gattatttgt ggctcacctg aaggetttgc aaaatttgta ccataaccgt 1320  
ttatttaaca tatattttta tttttgattg cacttaaat ttgtataatt tgtgtttctt 1380  
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
tagtgggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500  
gcactctgtt ttcctgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta ccacaaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159





<400> 163  
cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120

```

attgtttcgc tggtcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccctttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttaca cagcaacctc 360
ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
caggggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
tatgcagaat tctgtacca aattggcctt ttggatgaga agcaaaaaaa gtacttccag 900
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggctttgaa 960
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080
tatgtgaaat tttgtcact cccagaggtg agacaaggca tccacgtggg gaatcagact 1140
tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200
ccatgggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260
atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320
caggaataca agaaggcaga aaaaaaagtt tggagatct ttaaactctg cagtgaagtg 1380
gctggttaca tccggcaagc ggggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500
aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620
tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
ttttagggtc ttgaatagga agtttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860
taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920
gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

```

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

```

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
  1                   5                   10                   15

```

```

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
                20                   25                   30

```

```

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
  35                   40                   45

```

```

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
  50                   55                   60

```

```

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```

65				70				75				80				
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln	
				85					90					95		
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro	
				100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val	
				115					120					125		
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr	
				130					135					140		
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser	
				145					150					155		
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala	
				165					170					175		
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu	
				180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys	
				195					200					205		
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg	
				210					215					220		
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser	
				225					230					235		
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile	
				245					250					255		
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His	
				260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu	
				275					280					285		
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr	
				290					295					300		
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys	
				305					310					315		
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro	
				325					330					335		
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly	
				340					345					350		

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctggatcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggtctt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60  
 atttttccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120  
 tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180  
 tccttgcttc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtggagt 240  
 gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300  
 cctggagagc ctgggggagg gctgcctaa caagctttca aaaaacagga gcgacttcca 360  
 ctgggctggg ataagacgtg ccggtaggat aggggaagact gggtttagtc ctaatatcaa 420  
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaacagatgg 480  
 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540  
 tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600  
 gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
 accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccggaaa ttatttttgg 720  
 tctgaccact ctgccttggt ttttgcagaa tcatgtgagg gccaacgggg gaaggtggag 780  
 cagatgagca cacacaggag ccgtctcctc accgccgccc ctctcagcat ggaacagagg 840  
 cagccctggc cccgggccct ggaggtggac agccgctctg tggctcctgt ctcagtgggc 900  
 tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960  
 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020  
 ggggccatca accgggtcta taagctgaca ggcaacctga ccatccaggt ggctcataag 1080  
 acagggccag aagaggacaa caagtctcgt taccgcccc tcatcgtgca gccctgcagc 1140  
 gaagtgtca ccctcaccaa caatgtcaac aagctgtcga tcattgacta ctctgagaac 1200  
 cgctgtctgg cctgtgggag cctctaccag ggggtctgca agctgtgag gctggatgac 1260  
 ctcttcatcc tgggtgagcc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320  
 acgggaccca tgtacgggtg gattgtgcgc tctgaggggt aggatggcaa gctcttcac 1380  
 ggacggctg tggatgggaa gcaggattac ttcccgaccc tgtccagccg gaagctgcc 1440  
 cgagaccctg agtcctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500  
 ctcatcaaga tcccttcaga caccctggcc ctggtctccc actttgacat cttctacatc 1560  
 tacggctttg ctagtggggg ctttgtctac tttctcactg tccagccgga gaccctgag 1620  
 ggtgtggcca tcaactccgc tggagacctc ttctacacct caccgatcgt gcggctctgc 1680

```

aaggatgacc ccaagttcca ctcatacgtg tccctgccct tcggtgcac ccgggcccgg 1740
gtggaatacc gctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
cagtatcacc acccgccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920
ttgcagatca aggagcgct gcagtctgc taccagggcg agggcaacct ggagctcaac 1980
tggctgctgg ggaaggacgt ccagtgcacg aaggcgctg tccccatcga tgataacttc 2040
tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160
gtgggttttg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220
tgctccaatg ccattcacct cctcagcaaa gagtccctct tggaaggtag ctattggtgg 2280
agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaga 2340
aggggttaat tttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400
gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaact ttaagaagg 2460
acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1             5             10             15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20             25             30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35             40             45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50             55             60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65             70             75             80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85             90             95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100            105            110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115            120            125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130            135            140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145            150            155            160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165            170            175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450	455	460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr		
465	470	475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly		
	485	490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val		
	500	505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys		
	515	520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln		
	530	535 540
Leu Tyr Phe Leu Gly Glu Gln Arg		
545	550	

&lt;210&gt; 171

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 171

tggaataccg cctcctgcag

20

&lt;210&gt; 172

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 172

cttctgccct ttggagaaga tggc

24

&lt;210&gt; 173

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctccccg gcgcggctga gtgcggactg gagggggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggtctc ctgggtgctc gcaggctgga ctggagcacc ctgggtccctc 180  
tgcggtcccg ccatcgacag ctggggctgc aggccaaaggg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactatit ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggccctc 480  
acatctgcag tgagatggac ctcgggggct tgcccagctg gctactccaa gacctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat tttgaccacc 600  
tgatgtccag ggtggtgcc ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagaaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccagga gtcttgacca ccatcaactt gcagtcaaca cagagctgc 840  
agctactgac cacccttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900  
actggacggg gtggtttgac tcgtggggag gccctcaca tatcttggat tctctgagg 960  
ttttgaaaac cgtgtctgcc attgtggacg ccggtcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcatgaatg gagccatgca cttccatgac tacaagtcag 1080  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttcggtcca tctcaggcat cctctccct ccccccactg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
acgccctcaa gtacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320  
tgccagtcaa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380  
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcagggtgtt gtgaacacag 1440  
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680  
ggngttccct ccagaaaca cccacattac ctgcttctt cttgggtagc ttgtccatca 1740  
gtccacgcc ttgtgacacc tttctgaagc tggaggctg ggagaagggg gttgtattca 1800  
tcaatggcca gaaccttga cgttactgga acattggacc ccagaagacg ctttacctcc 1860  
caggctccgt gttgagcagc ggaatcaacc agctcatcgt tttgaggag acgatggcgg 1920  
gccctgcatt acagttcacg gaaaccccc accctggcag gaaccagtac attaatgag 1980  
cggtggcacc cctcctgct ggtgccagt ggagactgcc gcctcctctt gacctgaagc 2040  
ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aaacctcagg 2100  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg 2160  
ggatggctct gggcctggct ttgttgatga tggttttct acagccctgc tcttgtgcg 2220  
aggctgtcgg gctgtctcta ggggtggagc agctaatac atcgcccagc ctttggccct 2280

```

cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcctctgctg 2340
gactcaggcg tgctctttgc tggttcctgg gaggttggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttccccctt tcccttccca ctcgctgctt cccacagggt 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggtg 2640
ctctggtgtt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggccagct 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1                      5                      10                      15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
                20                      25                      30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
    35                      40                      45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
    50                      55                      60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
    65                      70                      75                      80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
                85                      90                      95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
    100                      105                      110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
    115                      120                      125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
    130                      135                      140

```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

```

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60
ccctggtgag gggtctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggcccaggg ccccaggac ctccatctcc caatgttga 180
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaagccca 240
tggtcccaa gaagctgtcc tgccttcgtt ccctgtgtgt gccgtcagc ctgacgttac 300
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360
tagacggggc cccgttcgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

```

```

tgctttgggc cgaccggcctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccttg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660
ctgaaattca tctaagaacc tcagatccag acttcccttg cgcagtggac tcctggttca 720
aggtcttgct gcccaagata tatccatggc tttatcacaa tgggggcaac atcattagca 780
ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840
tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
ctgacaacat gacccaaaatc tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020
taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080
ctgtgtcagc tgtaacccaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtgccat aagaaggagc 1200
gcttccctcc gattactacc agctatgact atgatgcacc tatactctgaa gcaggggacc 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320
gacctttacc tcccccgagc cccaagatga tgcctggacc tgtgactctg cactcgtttg 1380
ggcatttact ggctttccta gacttgcttt gcccccgagg gccattcat tcaatcttgc 1440
caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga acctatatga 1500
cccataccat ttttgagcca acaccattct ggggtgccaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620
tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680
tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800
ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980
ggccacaaca gaccctctac gtgccaaagat tcctgctgtt tcctagggga gccctcaaca 2040
aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
atacactgag tgcccttgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
aaattagccg ggcgtgatg gggtcacctc taatcccagc tacttgggag gctgagggca 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagtga tggaggttgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaaa 2505

```

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

```

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1              5              10             15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
          20              25             30

```

```

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
  35              40             45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
  50              55             60

```

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

	340		345		350
Ser	Lys Phe Gln Glu Val	Pro Leu Gly Pro Leu	Pro Pro Pro Ser	Pro	
	355	360	365		
Lys	Met Met Leu Gly Pro Val	Thr Leu His Leu Val	Gly His Leu Leu		
	370	375	380		
Ala	Phe Leu Asp Leu Leu Cys	Pro Arg Gly Pro Ile	His Ser Ile Leu		
385		390	395		400
Pro	Met Thr Phe Glu Ala Val	Lys Gln Asp His Gly	Phe Met Leu Tyr		
		405	410	415	
Arg	Thr Tyr Met Thr His Thr	Ile Phe Glu Pro Thr	Pro Phe Trp Val		
		420	425	430	
Pro	Asn Asn Gly Val His Asp	Arg Ala Tyr Val Met	Val Asp Gly Val		
	435	440	445		
Phe	Gln Gly Val Val Glu Arg	Asn Met Arg Asp Lys	Leu Phe Leu Thr		
	450	455	460		
Gly	Lys Leu Gly Ser Lys Leu	Asp Ile Leu Val Glu	Asn Met Gly Arg		
465		470	475		480
Leu	Ser Phe Gly Ser Asn Ser	Ser Asp Phe Lys Gly	Leu Leu Lys Pro		
		485	490	495	
Pro	Ile Leu Gly Gln Thr Ile	Leu Thr Gln Trp Met	Met Phe Pro Leu		
		500	505	510	
Lys	Ile Asp Asn Leu Val Lys	Trp Trp Phe Pro Leu	Gln Leu Pro Lys		
	515	520	525		
Trp	Pro Tyr Pro Gln Ala Pro	Ser Gly Pro Thr Phe	Tyr Ser Lys Thr		
	530	535	540		
Phe	Pro Ile Leu Gly Ser Val	Gly Asp Thr Phe Leu	Tyr Leu Pro Gly		
545		550	555		560
Trp	Thr Lys Gly Gln Val Trp	Ile Asn Gly Phe Asn	Leu Gly Arg Tyr		
		565	570	575	
Trp	Thr Lys Gln Gly Pro Gln	Gln Thr Leu Tyr Val	Pro Arg Phe Leu		
		580	585	590	
Leu	Phe Pro Arg Gly Ala Leu	Asn Lys Ile Thr Leu	Leu Glu Leu Glu		
	595	600	605		
Asp	Val Pro Leu Gln Pro Gln	Val Gln Phe Leu Asp	Lys Pro Ile Leu		
	610	615	620		

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178  
 tggctactcc aagaccctgg catg 24

<210> 179  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179  
 tggacaaatc cccttgctca gccc 24

<210> 180  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180  
 gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg 50

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181  
 ccagctatga ctatgatgca cc 22



<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcacccag aatggtggtg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattat 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cttttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcggt 300  
 ttggtgtggt cttgtcagaa gttagtgaata ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420  
 tgcatctgtt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgccctcacg tgaagttcac tgatgtgggt gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagtccctt ccaacattac agatgtgggt ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc cttaagaaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattctctcc tctattaccc atgtcaaaaa cttggagtcg ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcatatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaaag tggacattct gccaaaacaa ttgttttaaat 1320

```

gcataaaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500
tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
ttgcaaatgg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
ctttttaaataaaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta ggggttttaag tcattcattt ccaaattcatt tttttttttc ttttggggaa 1800
agggaaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggtat 1860
gctgccgcta ctgaatgttt acaaattgct tgccctgctaa agtaaatgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaaa 1947

```

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

```

```

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
          20             25             30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
          35             40             45

```

```

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
          50             55             60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
          65             70             75             80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
          85             90             95

```

```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
          100             105             110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
          115             120             125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
          130             135             140

```

```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
          145             150             155             160

```

```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
          165             170             175

```

```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
          180             185             190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465                      470                      475                      480  
 Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
                          485                      490                      495  
 Phe Ala Asn Gly Ile  
                          500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c 21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg 24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60  
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120  
 aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctcccttg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
 gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300  
 atcgctgggtg gtatcctggc ggccttgctc ctgctgatat ttgtcgtgct ctgtcctttac 360  
 ttcaaaatac acaacgcgct aaaagctgca aaggaaacctg aagctgtggc tgtaaaaaat 420  
 cacaacccag acaaggtgtg gtgggccaaag aacagccagg ccaaaacccat tgccacggag 480  
 tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
 ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
 cagctgctgg agatccctac agagagcttc cactgggggc aaccttcca ggaaggagt 780  
 ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctacctctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tcggtcctta aggctgcccc gcgcttgcc 960  
 aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctggttgccg 1020  
 gagctgacaa tggcgaggc tgaaggcaat gcaagctgca cagtcagtc aggggggacc 1080  
 aatagggcag agaccacaa agccatgatc ctgcaactca atcccagtg gaactgcacc 1140  
 tggacaaatg aaagaccaga aaacaaaagc atcagaatta tcttttctta tgtccagctt 1200  
 gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320  
 tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
 gtcttctact acttcttctc tctaacatc tctattccaa actgtggcgg ttacctggat 1440  
 accttggaag gatccttcac cagccccaat tacccaaagc cgcacctga gctggcttat 1500  
 tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
 ttcctagaaa tagacaaaca gtgcaaattt gattttcttg ccatctatga tggccctcc 1620  
 accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccacctt cgaatcgtca 1680  
 tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
 gcttctaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800  
 gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc taatgggaat 1860  
 aacttgcaac taaaagacc aacttgca ccaaaattat caaatgtgt ggaattttct 1920  
 gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
 aatataatca ccttttctgc atctcaact tctgaagtga tcaccctca gaaacaactc 2040  
 cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
 gaagatgatg taatacaaa tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160  
 tttgaatcca attcatttga aaagactata ctggaatcac catattatgt ggatttgaac 2220  
 caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280  
 gatacctgta gagcctctcc cactctgac ttgtcatctc caacctacga cctaatacaag 2340  
 agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaac ctatgggaga 2400  
 ttcagttta atgcctttta attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
 gttttgatat gtgatagcag tgaccaccag tctcgctgca atcaagggtg tgtctccaga 2520  
 agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580  
 ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640  
 gaaactccaa accagccttt caacagtgtg catctgtttt ccttcaggt tctagctctg 2700  
 aatgtgggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggagactac 2760  
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggctgaaag tgacacacag gcctgcatgt aaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
			580					585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
			595				600					605			

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120  
 ctgctgctgc cgccgcgcgc gtgcctgcc cacagcgcca cgcgcttcga cccacctgg 180



```

gagtcacctgg acgcccgcga gctgcccgcg tggtttgacc aggcccaagtt cggcatcttc 240
atccactggg gagtgttttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360
aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgcaa ccagtgggca 420
gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccaag 540
agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttgga 600
ctgtactatt ccctttttga atggtttcat ccgctcttcc ttgaggatga atccagtcca 660
ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtatgc 840
accaatgate gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960
aaactgtcct ggggctatag gagggaagct ggaatctctg actatcttac aattgaagaa 1020
ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaattattgg 1080
cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtggggtcc 1140
tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200
actgtcaccc catagtgtgt gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260
tttcttaaat ggccacatc aggacagctg ttccttggcc atcccaaagc tattctgggg 1320
gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380
aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500
atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620
ttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680
cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattggtgg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800
tatatagtta tgcatactt aatatgggga ttttttctgg gaaatgcatt gctagtcaat 1860
ttttttttgt gccacatca tagagtgtat ttacaaaatc ctatagtgca tagcctacta 1920
cacaccta atgtgatggt tagactgttg ctcttaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040
gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtga tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aattttttaa accttttttg ctcttttgta ataacttta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

```

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu

1

5

10

15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr

20

25

30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

35

40

45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgccagc atcagccact ctgc

24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca

45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttccctgg ctctgaagggt gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcaattccat ctggaccacg aggtcctctg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccagggt gtcatgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtggtcatt tctaggatta gcccaaacc ccaagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttgaag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720  
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 tttggtgctg cagctgggtc tggattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960  
 tttcaaaaca agaactcagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaaccc agaagagtcc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tggtttcttt catgctcctt accctgcccc agctggggaa 1200  
 atcaaaaggg ccaagaagacc aaagaagaaa gtccaccctt ggttcctaac tggaaatcagc 1260  
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320  
 cctgtctgga tcctatcctc ctacctccaa agcttccac ggcctttcta gcctggctat 1380  
 gtccctaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctagggtg gggtgaaagc 1500
caaggagtca ctgagaccaa ggcttttctct actgattccg cagctcagac ccttttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga caggggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgttttag aacacacaca cttacttttt ctggtctcta ccactgctga tatttttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgttttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct ggggaagctat 2100
ttttttcagt tttgatattt ctagcttata tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca catttttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1              5              10              15

```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20              25              30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35              40              45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50              55              60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65              70              75              80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85              90              95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
     100              105              110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
     115              120              125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
     130              135              140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 203  
 gtcagtgaca gtacctactc gg 22

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 204  
 tggagcagga ggagtagtag tagg 24

<210> 205  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 205  
 aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206  
 <211> 1620  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (973)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (977)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (996)  
 <223> a, t, c or g

<220>  
 <221> modified\_base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccttgccttc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc caccgtctgc ccaccaacg cgaagacggt aaccctgttg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttggata ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
tggagtcttt tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgagca catcacccct caccaagcaa ctccctacc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgcggcgggc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaattgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggcttcaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttccctc cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttctactg gagcaagaaa gagatctcat aggacggagg gggaaatgg 1140
ttccctcaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccctaa gcccttctgg ctctgcttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatccct ggactttcac taacctctg 1560
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttcctttt 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80



Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
                             145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
                             225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

&lt;210&gt; 208

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 208

gcttgatattcgcattgggcctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcttgcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggg 120  
 cccattgctc ctgctgccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggctcatggc aaagacctcc ttaatggagt 240  
 gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccctgc cgtaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360  
 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420  
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggg 600

```

ctttccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660
ctgtgcagag caggctgcgg tggtagcctc ctttgagcag ctcttccggg cctgggagga 720
gggcctggac tggtagaacg cgggctggct gcaggatgct acggtgcagt accccatcat 780
gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840
ccgccaccgc cgcctgcacc gctatgatgt attctgcttc gctactgccc tcaaggggcg 900
ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960
ggaagatgat gccacgatcg ccaaggtggg acagctcttt gccgcctgga agttccatgg 1020
cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080
cccgcacctc aactgtgggc cccagagacc tggggctcga agctttggct tccccgacc 1140
gcagagccgc ttgtacggtg tttactgcta ccgccagcac taggacctgg ggccctcccc 1200
tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260
agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacad tttttacta 1320
ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380
aatcatgctt gctcccctgg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440
atccaggctg gtctccctcc ctttaaggagg ttggtgcccc gagtgggagg tggcctgtct 1500
agaatgccgc cgggagtcgc ggcatgggtg gcacagttct ccctgcccct cagcctgggg 1560
gaagaagagg gcctcggggg cctccggagc tgggcttttg gcctctcctg cccacctcta 1620
cttctctgtg aagccgctga cccagctctg cccactgagg ggctagggtt ggaagccagt 1680
tctaggcttc caggcgaaat ctgagggaag gaagaaactc cctccccgt tccccctccc 1740
ctctcggttc caaagaatct gttttgttgt catttgtttc tctgttttc ctgtgtgggg 1800
aggggccctc aggtgtgtgt actttggaca ataatgggtg ctatgactgc cttccgccaa 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa                                           1985

```

<210> 213  
<211> 360  
<212> PRT  
<213> Homo sapiens

<400> 213  
Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
1 5 10 15  
Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
20 25 30  
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
35 40 45  
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
50 55 60  
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
65 70 75 80  
Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
85 90 95  
Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
100 105 110  
Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115					120					125								
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr			
130					135					140								
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu			
145					150					155					160			
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg			
					165					170					175			
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala			
					180					185					190			
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly			
					195					200					205			
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr			
					210					215					220			
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro			
					225					230					235		240	
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp			
					245					250					255			
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu			
					260					265					270			
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu			
					275					280					285			
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys			
					290					295					300			
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser			
					305					310					315		320	
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu			
					325					330					335			
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr			
					340					345					350			
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His											
					355					360								

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttggtg gggtggag 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtgcg gaaatgcg 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ggagagcggg gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60  
 gcttctgttg ctactgaggg acggggccca ggggaagcca tcccagacg caggccctca 120  
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180  
 cggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgcgggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcggtag cgcgcctgg gacacgtacg acacggaccg 420  
 cgacgggct gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
 gcggcgcttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttcctg caccgccagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660  
 ggaggacctg gacagaaaca aagatggcta tgtccagggt gaggagtaca tcgcggatct 720  
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggcccactg 840  
 ggtgctgccc cctgccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggttaatt ggaacatggt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020  
 agcaccgcgc acctgccaca gcctcagagg cccgcacaat gaccggagga ggggccgctg 1080  
 tgggtctggc ccctccctgt ccaggccccg caggaggcag atgcagtccc aggcatactc 1140  
 ctgcccctgg gctctcaggg accccctggg tcggcttctg tcctgtcac acccccaacc 1200  
 ccaggagggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260  
 cagcccagac ccagggaccc ttggcccaa gctcagctct aagaaccgcc ccaaccctc 1320  
 cagctccaaa tctgagctc caccacatag actgaaactc ccctggcccc agccctctcc 1380  
 tgcttggcct ggcttgggac acctcctctc tgccaggagg caataaaagc cagcgcgggg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 ggggccttgc cttccgcact cggggcgcage cgggtggatc tcgagcaggt gcgagagcccc 60  
 gggcggcggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120  
 ccagcctgtc tgtcgtcggt ttggcgcccc cgcctccccg cgggtgcgggg ttgcacaccg 180  
 atcctgggct tcgctcgatt tgccgcgcag gcgcctccca gacctagagg ggcgctggcc 240  
 tggagcagcg ggtcgtctgt gtccctctctc ctctgcgcgc cgcgcgggga tccgaagggt 300  
 gcggggctct gaggaggtga cgcgcggggc ctcccgcaacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggtc 420  
 tggcctcgg tgtgtgtctg ctgctgctgc cggggcccg gggcagcgag ggagccgctc 480  
 ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540  
 tctgcccagg gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgctt 600  
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660  
 ctgtacgagt ctatagccta cctggtcgag aaaactattc ctacgtagat gccaatggca 720  
 tccagtctca aatgctttct agatggtctg cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtggt ccacagcaca tccaccaaca ggtaaacgac 840  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
 tgtttgccat aaaggaagta ggtttcagag ggggttaatt caatacagga aaagccttga 1140  
 agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atcccccagg 1200  
 tgggtggtgg atttattgat ggttggcctt ctgatgacat cgaggaagca ggcattgttg 1260  
 ccagagagtt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320  
 tggggatggg tcaggatgtc acatttgttg acaaggctgt ctgtcggaat aatggcttct 1380  
 tctcttacca catgccccac tgggttggca ccacaaaata cgtaaagcct ctggtacaga 1440  
 agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500  
 cctttctaata tgatggctcc agcagtggtg gagatagcaa tttccgcctc atgcttgaat 1560  
 ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620  
 tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680  
 atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggaaacagct actggtgatg 1740  
 ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800  
 tcctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860  
 cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920  
 tgaaagatat ggcttctaaa ccgaaggagt ctcacgcttt cttcacaaga gatttcacag 1980  
 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040  
 agcaataatt gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100  
 attgtattct cataaactg aaatgcttta gcatactaga atcagataca aaactattaa 2160  
 gtatgtcaac agccatttag gcaaataagc actcctttta agccgctgcc ttctgggttac 2220  
 aatttacagt gtactttggt aaaaacactg ctgaggcttc ataactatgg ctcttagaaa 2280  
 ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340  
 tgtacagata tgcaaattcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaaa 2400  
 aaa 2403

<210> 227

<211> 550  
 <212> PRT  
 <213> Homo sapiens

<400> 227

```

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
  1           5           10           15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
          20           25           30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
          35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
          50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
          65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
          85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
          100          105          110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
          115          120          125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
          130          135          140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
          145          150          155          160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
          165          170          175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
          180          185          190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
          195          200          205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
          210          215          220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
          225          230          235          240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
          245          250          255

```

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
tggtctcgca caccgatc 18

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229  
ctgctgtcca caggggag 18

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
ccttgaagca tactgctc 18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa tttccgcc 18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttcctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga tttc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 cgccgcgctc ccgcacccgc ggcccgccca ccgcgcgct cccgcatctg caccgcagc 60  
 ccggcgccct ccggcgggga gcgagcagat ccagtccggc ccgcagcgca actcgggtcca 120  
 gtcggggcgcg cggtctcggg cgagagcgg agatgcagcg gcttggggcc accctgctgt 180  
 gctgctgctt ggcggcggcg gtccccacgg cccccgcgct cgctccgacg gcgacctcgg 240  
 ctccagtcga gcccgggccc gctctcagct acccgagga ggaggccacc ctcaatgaga 300  
 tgttcgcgga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540  
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcg 600  
 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

```

gtgtctgggg tcaactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780
accagagggga ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccttg 840
tgtgcacacc cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttcttg 900
acctcatcac ctgggagcta gagcctgatg gagccttggg ccgatgccct tgtgccagt 960
gcctcctctg ccagccccac agccacagcc tgggtgatgt gtgcaagccg accttcgtgg 1020
ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtccccgat gagtatgaag 1080
ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140
aagagatggc gctgggggag cctgcccgtg ccgcgcgtgc actgctggga ggggaagaga 1200
tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt tatttcccca 1260
gggtgtgtgt ttaggcgtgg gctgaccagg cttcttccca catcttcttc ccagtaagtt 1320
tcccctctgg cttgacagca tgagggtgtt tgcatttgtt cagctccccc aggctgttct 1380
ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaaactgca ggagcagttt 1440
gccacccttg tccagattat tggtgcttt gcctctacca gttggcagac agccgtttgt 1500
tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560
tgattggttt tggggaaatg tggagaagag tgccctgctt tgcaaacatc aacctggcaa 1620
aaatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680
cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740
gtgttgctca gtcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc 1800
tctctcagca cagcctgggg aggggggtcat tgttctcctc gtccatcagg gatctcagag 1860
gctcagagac tgcaagctgc ttgcccaggt cacacagcta gtgaagacca gagcagtttc 1920
atctggttgt gactctaagc tcagtgtctt ctccactacc ccacaccagc cttggtgcca 1980
ccaaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040
attaaggtca aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160
ctttggcagt tgcattagta actttgaaaag gtatatgact gagcgtagca tacagggttaa 2220
cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280
cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340
tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460
taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520
aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
aaaaaa

```

&lt;210&gt; 236

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

```

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
  1                      5                      10                      15

```

```

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
                20                      25                      30

```

```

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
        35                      40                      45

```

```

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50                      55                      60

```

```

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
    65                      70                      75                      80

```

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
325 330 335

Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
340 345 350

&lt;210&gt; 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 ggagctgcac cccttgc 17

<210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 238  
 ggaggactgt gccacatga gagactcttc aaaccaagg caaaattgg 49

<210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 239  
 gcagagcggg gatgcagcgg ctg 24

<210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 240  
 ttggcagctt catggagg 18

<210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 241  
 cctgggcaaa aatgcaac 18



<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg

45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50  
 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacataca 150  
 cacacataca ccttctcttc cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcttgccc 250  
 attacctctg cagctccttt ggcttggtga gtcaaaaaac atgggagggg 300  
 ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350  
 tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

ggggtagata ctgcttctct gcaacctcct taactctgca tcctcttctt 650  
 ccagggtctgc ccctgatggg gcctggcaat gactgagcag gccagcccc 700  
 agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccc 750  
 gtgtagaatg actgccctgg gaggggtggtt ccttgggccc tggcagggtt 800  
 gctgaccctt accctgcaaa acacaaagag caggactcca gactctcctt 850  
 gtgaatggtc ccctgccctg cagctccacc atgaggettct tctggtgcccc 900  
 actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggtac 950  
 cctggcatgt tccctgcccc cctcagtgtg cctgccagat ccggccctgg 1000  
 tatacgcccc gctcgtccta ccgcgaggct accactgtgg actgcaatga 1050  
 cctattcctg acggcagctc ccccggcact ccccgcaggc acacagacct 1100  
 tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150  
 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200  
 tgcccagagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250  
 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggtctg 1300  
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350  
 ccccagggcc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400  
 ccaacctcct gagggccatt gacagccgtt ggtttgaaat gctgcccac 1450  
 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500  
 gaacttccgg cccctggcca acctgcgtag cctggtgcta gcaggcatga 1550  
 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600  
 agcctctcct tctatgacaa ccagctggcc cgggtgccc aagcgggact 1650  
 ggaacagggtg cccgggctca agttcctaga cctcaacaag aaccgctcc 1700  
 agcgggtagg gccgggggac tttgccaaac tgctgcacct taaggagctg 1750  
 ggactgaaca acatggagga gctggtctcc atcgacaagt ttgccctggt 1800  
 gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850  
 ccttcatcca ccccgcgcc ttccaccacc tgccccagat ggagaccctc 1900  
 atgctcaaca acaacgctct cagtgccttg caccagcaga cgggtggagtc 1950

cctgcccac	ctgcaggagg	taggtctcca	cggcaacccc	atccgctgtg	2000
actgtgtcat	ccgctggggc	aatgccacgg	gcacccgtgt	ccgcttcac	2050
gagccgcaat	ccaccctgtg	tgcggagcct	ccggacctcc	agcgccctcc	2100
ggtccgtgag	gtgcccttcc	gggagatgac	ggaccactgt	ttgcccctca	2150
tctccccacg	aagcttcccc	ccaagcctcc	aggtagccag	tggagagagc	2200
atggtgctgc	attgccgggc	actggccgaa	cccgaacccg	agatctactg	2250
ggtcactcca	gctgggcttc	gactgacacc	tgcccatgca	ggcaggagggt	2300
accgggtgta	ccccgagggg	accctggagc	tgcggaggggt	gacagcagaa	2350
gaggcagggc	tatacacctg	tgtggcccag	aacctggtgg	gggctgacac	2400
taagacgggt	agtgtgggtg	tgggccgtgc	tctcctccag	ccaggcaggg	2450
acgaaggaca	ggggctggag	ctccgggtgc	aggagaccca	cccctatcac	2500
atcctgctat	cttgggtcac	cccacccaac	acagtgtcca	ccaacctcac	2550
ctggtccagt	gcctcctccc	tccggggcca	ggggggccaca	gctctggccc	2600
gcctgcctcg	gggaacccac	agctacaaca	ttaccgcct	ccttcaggcc	2650
acggagtact	gggcctgcct	gcaagtggcc	tttgctgatg	cccacacca	2700
gttggtctgt	gtatggggcca	ggaccaaaga	ggccacttct	tgccacagag	2750
ccttagggga	tcgctcctggg	ctcattgcca	tcctggctct	cgctgtcctt	2800
ctcctggcag	ctgggctagc	ggcccacctt	ggcacaggcc	aaccacaggaa	2850
gggtgtgggt	gggagggcgg	ctctccctcc	agcctgggct	ttctggggct	2900
ggagtgcctc	ttctgtccgg	gttgtgtctg	ctccccctcg	cctgccttgg	2950
aatccaggga	ggaagctgcc	cagatcctca	gaaggggaga	cactgttgcc	3000
accattgtct	caaaattctt	gaagctcagc	ctgttctcag	cagtagagaa	3050
atcactagga	ctacttttta	ccaaaagaga	agcagtctgg	gccagatgcc	3100
ctgccaggaa	agggacatgg	acccacgtgc	ttgaggcctg	gcagctgggc	3150
caagacagat	ggggctttgt	ggccctgggg	gtgcttctgc	agccttgaaa	3200
aagttgcct	tacctcctag	ggtcacctct	gtgcatttc	tgagggaacat	3250

ctccaaggaa caggagggac tttggctaga gcctcctgcc tccccatctt 3300  
ctctctgccc agaggctcct gggcctggct tggctgtccc ctacctgtgt 3350  
ccccgggctg cacccttccc tcttctcttt ctctgtacag tctcagttgc 3400  
ttgctcttgt gcctcctggg caagggctga aggaggccac tccatctcac 3450  
ctcggggggc tgccctcaat gtgggagtga cccagccag atctgaagga 3500  
catttgggag agggatgccc aggaacgect catctcagca gcctgggctc 3550  
ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly
1				5					10					15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro
				20					25					30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
				35					40					45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
				50					55					60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
				65					70					75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
				80					85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
				95					100					105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
				110					115					120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
				125					130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
				140					145					150

Asn Gln Leu Tyr Arg	Ile Ala Pro Arg	Ala Phe Ser Gly Leu Ser
155	160	165
Asn Leu Leu Arg Leu	His Leu Asn Ser	Asn Leu Leu Arg Ala Ile
170	175	180
Asp Ser Arg Trp Phe	Glu Met Leu Pro	Asn Leu Glu Ile Leu Met
185	190	195
Ile Gly Gly Asn Lys	Val Asp Ala Ile	Leu Asp Met Asn Phe Arg
200	205	210
Pro Leu Ala Asn Leu	Arg Ser Leu Val	Leu Ala Gly Met Asn Leu
215	220	225
Arg Glu Ile Ser Asp	Tyr Ala Leu Glu	Gly Leu Gln Ser Leu Glu
230	235	240
Ser Leu Ser Phe Tyr	Asp Asn Gln Leu	Ala Arg Val Pro Arg Arg
245	250	255
Ala Leu Glu Gln Val	Pro Gly Leu Lys	Phe Leu Asp Leu Asn Lys
260	265	270
Asn Pro Leu Gln Arg	Val Gly Pro Gly	Asp Phe Ala Asn Met Leu
275	280	285
His Leu Lys Glu Leu	Gly Leu Asn Asn	Met Glu Glu Leu Val Ser
290	295	300
Ile Asp Lys Phe Ala	Leu Val Asn Leu	Pro Glu Leu Thr Lys Leu
305	310	315
Asp Ile Thr Asn Asn	Pro Arg Leu Ser	Phe Ile His Pro Arg Ala
320	325	330
Phe His His Leu Pro	Gln Met Glu Thr	Leu Met Leu Asn Asn Asn
335	340	345
Ala Leu Ser Ala Leu	His Gln Gln Thr	Val Glu Ser Leu Pro Asn
350	355	360
Leu Gln Glu Val Gly	Leu His Gly Asn	Pro Ile Arg Cys Asp Cys
365	370	375
Val Ile Arg Trp Ala	Asn Ala Thr Gly	Thr Arg Val Arg Phe Ile
380	385	390
Glu Pro Gln Ser Thr	Leu Cys Ala Glu	Pro Pro Asp Leu Gln Arg
395	400	405
Leu Pro Val Arg Glu	Val Pro Phe Arg	Glu Met Thr Asp His Cys

410										415					420				
Leu	Pro	Leu	Ile	Ser	Pro	Arg	Ser	Phe	Pro	Pro	Ser	Leu	Gln	Val					
				425					430					435					
Ala	Ser	Gly	Glu	Ser	Met	Val	Leu	His	Cys	Arg	Ala	Leu	Ala	Glu					
				440					445					450					
Pro	Glu	Pro	Glu	Ile	Tyr	Trp	Val	Thr	Pro	Ala	Gly	Leu	Arg	Leu					
				455					460					465					
Thr	Pro	Ala	His	Ala	Gly	Arg	Arg	Tyr	Arg	Val	Tyr	Pro	Glu	Gly					
				470					475					480					
Thr	Leu	Glu	Leu	Arg	Arg	Val	Thr	Ala	Glu	Glu	Ala	Gly	Leu	Tyr					
				485					490					495					
Thr	Cys	Val	Ala	Gln	Asn	Leu	Val	Gly	Ala	Asp	Thr	Lys	Thr	Val					
				500					505					510					
Ser	Val	Val	Val	Gly	Arg	Ala	Leu	Leu	Gln	Pro	Gly	Arg	Asp	Glu					
				515					520					525					
Gly	Gln	Gly	Leu	Glu	Leu	Arg	Val	Gln	Glu	Thr	His	Pro	Tyr	His					
				530					535					540					
Ile	Leu	Leu	Ser	Trp	Val	Thr	Pro	Pro	Asn	Thr	Val	Ser	Thr	Asn					
				545					550					555					
Leu	Thr	Trp	Ser	Ser	Ala	Ser	Ser	Leu	Arg	Gly	Gln	Gly	Ala	Thr					
				560					565					570					
Ala	Leu	Ala	Arg	Leu	Pro	Arg	Gly	Thr	His	Ser	Tyr	Asn	Ile	Thr					
				575					580					585					
Arg	Leu	Leu	Gln	Ala	Thr	Glu	Tyr	Trp	Ala	Cys	Leu	Gln	Val	Ala					
				590					595					600					
Phe	Ala	Asp	Ala	His	Thr	Gln	Leu	Ala	Cys	Val	Trp	Ala	Arg	Thr					
				605					610					615					
Lys	Glu	Ala	Thr	Ser	Cys	His	Arg	Ala	Leu	Gly	Asp	Arg	Pro	Gly					
				620					625					630					
Leu	Ile	Ala	Ile	Leu	Ala	Leu	Ala	Val	Leu	Leu	Leu	Ala	Ala	Gly					
				635					640					645					
Leu	Ala	Ala	His	Leu	Gly	Thr	Gly	Gln	Pro	Arg	Lys	Gly	Val	Gly					
				650					655					660					
Gly	Arg	Arg	Pro	Leu	Pro	Pro	Ala	Trp	Ala	Phe	Trp	Gly	Trp	Ser					
				665					670					675					

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                   680                  685                  690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                   695                  700                  705

Leu Pro Pro Leu Ser Gln Asn Ser  
                   710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag gcgctgtttg agaaggtgaa gaagttccgg acccatgtgg 50

aggaggggga cattgtgtac cgctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcctctcat catctgtac accgtctact acgtgcacaa 150





acgctccctc cggagctctt ccagtgcggg aagctgcggg cctgcacct 1500  
gggcaacaac gtgctgcagt cactgccctc caggggtgggc gagctgacca 1550  
acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600  
gagctgggcg agtgcccact gctcaagcgc agcggccttg tggaggagga 1650  
ggacctgttc aacacactgc cccccgaggt gaaggagcgg ctgtggaggg 1700  
ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750  
gaccgctgcc cagtcctcag gcccgagggg gcaggcctag cttctcccag 1800  
aactcccgga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850  
gcttgtagt caggccagag cgagaggaca gtatctgtgg ggctggcccc 1900  
ttttctccct ctgagactca cgtccccag ggcaagtgt tgtggaggag 1950  
agcaagtctc aagagcgcag tatttgata atcagggtct cctccctgga 2000  
ggccagctct gccccagggg ctgagctgcc accagaggtc ctgggaccct 2050  
cactttagtt cttggtatct atttttctcc atctcccacc tccttcatcc 2100  
agataactta tacattccca agaaagtcca gccagatgg aaggtgttca 2150  
gggaaaggtg ggctgccttt tcccctgtc cttatttagc gatgccgccg 2200  
ggcatttaac acccacctgg acttcagcag agtgggccgg ggcgaaccag 2250  
ccatgggacg gtcaccacgc agtgccgggc tgggctctgc ggtgcgggtc 2300  
acgggagagc aggcctccag ctggaaaggc caggcctgga gcttgccctc 2350  
tcagtttttg tggcagtttt agttttttgt tttttttttt tttaatcaaa 2400  
aaacaatttt ttttaaaaaa aagctttgaa aatggatggg ttgggtatta 2450  
aaaagaaaaa aaaaacttaa aaaaaaaaag acactaacgg ccagtgagtt 2500  
ggagtctcag ggcagggtgg cagtttccct tgagcaaagc agccagacgt 2550  
tgaactgtgt ttcccttccc tgggagcagg gtgcagggtg tcttccggat 2600  
ctggtgtgac cttggtccag gaggttctatt tgttcctggg gagggaggtt 2650  
tttttgtttg ttttttgggt ttttttgggt tcttggtttt tttctcctcc 2700  
atgtgtcttg gcaggcactc atttctgtgg ctgtcgcca gagggaatgt 2750  
tctggagctg ccaaggaggg aggagactcg ggttggttaa tccccgatg 2800

aacggtgctc cattcgacc tcccctcctc gtgcctgccc tgccctctcca 2850  
 cgcacagtgt taaggagcca agaggagcca cttcgcccag actttgtttc 2900  
 cccacctcct ggggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950  
 cttccatcag cctgtgcgcc acctggctct tcatgaagag cagacactta 3000  
 gaggttggtc gggaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050  
 ccaagccggt tcccgctcct ggcgctgga gtgcacacag cccagtcggc 3100  
 acctggtggc tggaagccaa cctgctttag atcactcggg tccccacctt 3150  
 agaaggggtc cgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tottaatgat tatgtccatc cgtctgtccg tccatttgtg 3250  
 ttttctcgct cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccggt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400  
 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10				15	
Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
				20					25				30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40				45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55				60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70				75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85				90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys

95										100					105				
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro					
				110					115					120					
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu					
				125					130					135					
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp					
				140					145					150					
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu					
				155					160					165					
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp					
				170					175					180					
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val					
				185					190					195					
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu					
				200					205					210					
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala					
				215					220					225					
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp					
				230					235					240					
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu					
				245					250					255					
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr					
				260					265					270					
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu					
				275					280					285					
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp					
				290					295					300					
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr					
				305					310					315					
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr					
				320					325					330					
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser					
				335					340					345					
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn					
				350					355					360					

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

caacaatgag ggcaccaagc 20

&lt;210&gt; 252

&lt;211&gt; 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50  
 gcgctctccc gtcccgcggg ggttgctgct gctgccgctg ctgctgggcc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctgggtcatgt 250  
 ggcttcaggg cgggtccaggc ggttctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggetgcc agtctcctat ttgtggataa tcccggtgggc actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtaggt 450  
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca ttttctcaga gtctatgga ggaaaaatgg 550  
 cagctggcat tgggtctagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650  
 tgattcgggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800  
agaaatgatac attgaacaga acacagatgg ggtgaacttc tataacatct 850  
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
agatgcctta agccagctca tgaatggccc catcagaaaag aagctcaaaa 1000  
ttattcctga ggatcaatcc tggggaggcc aggctacca cgtctttgtg 1050  
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
tcgtagatac catgggtcag gaggcctggg tgcggaaaact gaagtggcca 1200  
gaactgccta aattcagtc gctgaagtgg aaggccctgt acagtgaccc 1250  
taaactcttg gaaacatctg cttttgtcaa gtcttacaag aaccttgctt 1300  
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
gggctggaga tgagctgggt tggccttggg gcacagagct gagctgaggc 1450  
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
ggaggcaatt tggaaattat ttctgcttct taaaaaacc taagattttt 1600  
taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10				15	
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20					25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	80	85	90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	95	100	105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	110	115	120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	125	130	135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	140	145	150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	170	175	180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	200	205	210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	215	220	225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	230	235	240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly			

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

```

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50
tgctgctggc tggggtgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tgagaggac gccgaactcg ggcgttgcc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagttagcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcc aacctctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```



```
<210> 257
<211> 314
<212> PRT
<213> Homo Sapien
```

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg  
1 5 10 15

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly  
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu  
80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
 290 295 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

[illegible]

tgatggctac tgggtgggtca gcaacagagt gccattoca tgggtgtccg 1450  
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg ccgccccct cttggctttc tcaacccaag 1550  
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600  
 atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggt 1650  
 cctggctggg atcctgtaac aggtctggga acaccaactt ccagctttg 1700  
 ctgaagactc tactcaacc ctgaccttt cctatcagga gagatggctt 1750  
 gtcccctgcc ctgaagctgg cagttcagtc ccttattctg ccctggtgga 1800  
 agccctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aacctgaaa tgctgtgagc ttgacttgac tccaacctt accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccaa ttactgcaa ggagacctct actgtcaccg 2100  
 tttactcttt cctacctga catccagaaa caatggcctc cagtgcatac 2150  
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300  
 tgtagatttt tgcctctctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaag taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1					5				10				15	

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

	20		25		30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	290	295	300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	305	310	315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	320	325	330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	335	340	345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

```

gccgcgcgct ctctcccggc gccacacct gtctgagcgg cgcagcgagc 50
cgcgggcccgg gcgggctgct cggcgcgga cagtgtctcg catggcaggg 100
attccagggc tctcttctct tctcttcttt ctgctctgtg ctgttgggca 150
agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggaaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttcctgtctc actacccttt ctcaacatca 550
gtgaagtat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcctaaagc ccaagtttaa agatggtggt 700
cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcttgctaa 900
gcagctgcc a gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

```

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggtgtcag aatcactcct ctcaaatacg ccagatttg 1200  
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggctctca tgttcttatt ttaggagagg 1300  
 ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactggcct tactatttga aaactgggtt gtgtatcata tcatatatca 1450  
 ttttaagcagt ttgaaggcat acttttgcag agaaataaaa aaaataactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1				5				10						15

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
			20					25						30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
			35					40						45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
			50					55						60

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
			65					70						75

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
			80					85						90

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
			95						100					105

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
			110					115						120



Ser Gly Lys Ser	Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile	Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val	Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His	Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val	Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe	Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro	Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val	Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys	Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly	Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn	Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu	Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly	Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg	Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn	Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp	Cys Arg Glu Gly	380		

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
 ccatgggtggg ttctggagcg ccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct cctgctgct gctggcgctg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca cactgcgca ggttctctgc tcaccagccg 300  
 ctgggtgatc actgctgcc actgtttcaa ggacaacctg aacaaccat 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
 cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctcgagcgt 500  
 ccatacagtt ctgagagcg gtctgcca tctgctacc tgatgcctct 550  
 atccacctcc ctccaaacac cactgctgg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccaccctca gacctgcag aagctgaagg 650  
 ttctatcat cgactcgga gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750  
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
 tggacggcgc ctggtgctg gccggcatca tcagctgggg cgagggtgt 850  
 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgcgcgcgc 1000  
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcggcctc gggcggtttc cccgcgcgta 1100  
 aataggctca tctacctcta cctctggggg ccgggacggc tgctgcggaa 1150

```
<210> 263
<211> 317
<212> PRT
<213> Homo Sapien
```

Met 1	Val	Val	Ser	Gly 5	Ala	Pro	Pro	Ala	Leu 10	Gly	Gly	Gly	Cys	Leu 15
Gly	Thr	Phe	Thr	Ser 20	Leu	Leu	Leu	Leu	Ala 25	Ser	Thr	Ala	Ile	Leu 30
Asn	Ala	Ala	Arg	Ile 35	Pro	Val	Pro	Pro	Ala 40	Cys	Gly	Lys	Pro	Gln 45
Gln	Leu	Asn	Arg	Val 50	Val	Gly	Gly	Glu	Asp 55	Ser	Thr	Asp	Ser	Glu 60
Trp	Pro	Trp	Ile	Val 65	Ser	Ile	Gln	Lys	Asn 70	Gly	Thr	His	His	Cys 75
Ala	Gly	Ser	Leu	Leu 80	Thr	Ser	Arg	Trp	Val 85	Ile	Thr	Ala	Ala	His 90
Cys	Phe	Lys	Asp	Asn 95	Leu	Asn	Lys	Pro	Tyr 100	Leu	Phe	Ser	Val	Leu 105
Leu	Gly	Ala	Trp	Gln 110	Leu	Gly	Asn	Pro	Gly 115	Ser	Arg	Ser	Gln	Lys 120
Val	Gly	Val	Ala	Trp 125	Val	Glu	Pro	His	Pro 130	Val	Tyr	Ser	Trp	Lys 135
Glu	Gly	Ala	Cys	Ala 140	Asp	Ile	Ala	Leu	Val 145	Arg	Leu	Glu	Arg	Ser 150
Ile	Gln	Phe	Ser	Glu 155	Arg	Val	Leu	Pro	Ile 160	Cys	Leu	Pro	Asp	Ala 165
Ser	Ile	His	Leu	Pro 170	Pro	Asn	Thr	His	Cys 175	Trp	Ile	Ser	Gly	Trp 180

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
				305					310					315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 266

agctctagac caatgccagc ttcc 24

<210> 267

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 267

gccaccaact cctgcaagaa cttctcagaa ctgccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 268

ggggaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggtc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgcatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggag actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100



agatgaggag	aaacgtttga	tgggtggagct	gcacaacctc	taccggggccc	150
aggatatcccc	gacggcctca	gacatgctgc	acatgagatg	ggacgaggag	200
ctggccgcct	tcgccaaggc	ctacgcacgg	cagtgcgtgt	ggggccacaa	250
caaggagcgc	gggcgccgcg	gcgagaatct	gttcgccatc	acagacgagg	300
gcatggacgt	gccgctggcc	atggaggagt	ggcaccacga	gcgtgagcac	350
tacaacctca	gcgccgccac	ctgcagccca	ggccagatgt	gcggccacta	400
cacgcaggtg	gtatgggcca	agacagagag	gatcggctgt	ggttcccact	450
tctgtgagaa	gctccagggt	gttgaggaga	ccaacatcga	attactggtg	500
tgcaactatg	agcctccggg	gaacgtgaag	gggaaacggc	cctaccagga	550
ggggactccg	tgctcccaat	gtccctctgg	ctaccactgc	aagaactccc	600
tctgtgaacc	catcggaagc	ccggaagatg	ctcaggattt	gccttacctg	650
gtaactgagg	ccccatcctt	ccgggcgact	gaagcatcag	actctaggaa	700
aatgggtact	ccttcttccc	tagcaacggg	gattccggct	ttcttggtaa	750
cagaggtctc	aggctccctg	gcaaccaagg	ctctgcctgc	tgtggaaacc	800
caggccccaa	cttccttagc	aacgaaagac	ccgccctcca	tggcaacaga	850
ggctccacct	tgcgtaacaa	ctgaggctcc	ttccattttg	gcagctcaca	900
gcctgccttc	cttggatgag	gagccagtta	ccttccccaa	atcgacccat	950
gttcctatcc	caaaatcagc	agacaaagtg	acagacaaaa	caaaagtgcc	1000
ctctaggagc	ccagagaact	ctctggacct	caagatgtcc	ctgacagggg	1050
caagggaact	cctaccccat	gcccaggagg	aggctgaggc	tgaggctgag	1100
ttgcctcctt	ccagtgaggt	cttggcctca	gtttttccag	cccaggacaa	1150
gccaggtgag	ctgcaggcca	cactggacca	cacggggcac	acctcctcca	1200
agtccttgcc	caatttcccc	aatacctctg	ccaccgctaa	tgccacgggt	1250
gggcgtgccc	tggctctgca	gtcgtccttg	ccagggtgcag	agggccctga	1300
caagcctagc	gttgtgtcag	ggctgaactc	ggggccctgg	catgtgtggg	1350
gccctctcct	gggactactg	ctcctgcctc	ctctggtggt	ggctggaatc	1400

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtctctctgt 1450  
 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650  
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
 tgccacacaca gcatgtgcgc tctccctgag tgctgtgta gctggggatg 1750  
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtggggg aggcagggac gaggggaagga aagtaactcc tgactctcca 1850  
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu					
1				5					10					15					
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp					
			20						25					30					
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala					
			35						40					45					
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp					
			50						55					60					
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val					
			65						70					75					
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe					
			80						85					90					
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu					
			95						100					105					
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys					
			110						115					120					
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala					
			125						130					135					

Lys Thr Glu Arg	Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu	140	145	150
Gln Gly Val Glu	Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr	155	160	165
Glu Pro Pro Gly	Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly	170	175	180
Thr Pro Cys Ser	Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser	185	190	195
Leu Cys Glu Pro	Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro	200	205	210
Tyr Leu Val Thr	Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser	215	220	225
Asp Ser Arg Lys	Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile	230	235	240
Pro Ala Phe Leu	Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys	245	250	255
Ala Leu Pro Ala	Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr	260	265	270
Lys Asp Pro Pro	Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr	275	280	285
Thr Glu Val Pro	Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu	290	295	300
Asp Glu Glu Pro	Val Thr Phe Pro Lys Ser Thr His Val Pro Ile	305	310	315
Pro Lys Ser Ala	Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser	320	325	330
Arg Ser Pro Glu	Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly	335	340	345
Ala Arg Glu Leu	Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu	350	355	360
Ala Glu Leu Pro	Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro	365	370	375
Ala Gln Asp Lys	Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr	380	385	390
Gly His Thr Ser	Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser	395	400	405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

tcattctcca agttatggtg gacgtacttc tgttgttctc cctctgcttg 100  
ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
attacacttc tctccttggc tggaaacagg attggtgaaa tactccctga 300  
acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350  
atatttcaga gctccaaact gcatttccag cctacagct caaatatctg 400  
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450  
tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500  
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctogaattg 550  
aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600  
tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650  
atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700  
aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750  
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850  
ttatcaagggt tagatgattc aagcttcctt ggccctaagct tactaaatac 900  
actgcacatt ggggaacaaca gagtcagcta cattgctgat tgtgccttcc 950  
gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000  
tggactattg aagacatgaa tgggtgctttc tctgggcttg acaaactgag 1050  
gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100  
tactgggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150  
atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200  
gcatttaaata acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250  
cacagtgggt ggcgaaaaac aactttcaga gctttgtaaa tgccagttgt 1300  
gcccacctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400  
 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450  
 gccagcagca gtgattcccc aatgactttt gcttggaata aagacaatga 1500  
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaag 1550  
 gtggcgaggt gatggagtat accaccatcc ttcggctgcg cgaggtggaa 1600  
 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttggttc 1650  
 atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700  
 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750  
 gagtgtgctg ctgtggggca cccagccccc cagatagcct ggcagaagga 1800  
 tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850  
 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900  
 gtatacagct gcacagctca gaacagtgc ggaagtattt cagcaaatgc 1950  
 aactctgact gtccatgaaa caccatcatt tttgoggcca ctgttgacc 2000  
 gaactgtaac caaggagaaa acagccgtcc tacagtgcac tgctggagga 2050  
 agccctcccc ctaaactgaa ctggacaaa gatgatagcc cattggtggt 2100  
 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150  
 actcagatgt cagtgatgct gggaaatata catgtgagat gtctaaccac 2200  
 cttggcactg agagaggaaa cgtgcgcctc agtgtgatcc ccactccaac 2250  
 ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300  
 ccactgtggg tgtcgtgatc atagccgtgg tttgctgtgt ggtgggcacg 2350  
 tcactcgtgt ggggtggtcat catataccac acaaggcgga ggaatgaaga 2400  
 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450  
 gttatttgtc atctcaggga acgttagctg acaggcagga tgggtacgtg 2500  
 tcttcagaaa gtggaagcca ccaccagttt gtcacatctt caggtgctgg 2550  
 atttttctta ccacaacatg acagtagtgg gacctgccat attgacaata 2600  
 gcagtgaagc tgatgtggaa gctgccacag atctgttctt ttgtccgttt 2650  
 ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tccttttgaa acatatcata caggttgcag tcctgacca agaacagttt 2750  
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctacca 2800  
 tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850  
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900  
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950  
 agtgcaaata cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000  
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag cctttttattt gaaagctcat 3100  
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaata acatttgtac ctttaaacag acttttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250  
 tgagaccaaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttattttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450  
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatagata 3500  
 taaatcatga ttattttatg tattttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600  
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650  
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25					30

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	
				35					40					45	
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	
				50					55					60	
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	
				65					70					75	
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	
				80					85					90	
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	
				95					100					105	
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	
				110					115					120	
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	
				125					130					135	
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	
				140					145					150	
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	
				155					160					165	
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	
				170					175					180	
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	
				185					190					195	
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	
				200					205					210	
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	
				215					220					225	
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	
				230					235					240	
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	
				245					250					255	
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	
				260					265					270	
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	
				275					280					285	
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	



290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro
560	565	570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro
575	580	585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val
590	595	600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser
605	610	615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr
620	625	630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu Asp
635	640	645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala
650	655	660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser
665	670	675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln
680	685	690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys Tyr
695	700	705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn Val
710	715	720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln Met
725	730	735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly Val
740	745	750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu Val
755	760	765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp Cys
770	775	780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile Pro
785	790	795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp Gly
800	805	810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
 1010 1015 1020  
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
 1025 1030 1035  
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
 1040 1045 1050  
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
 1055

<210> 291  
 <211> 2906

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

```

ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50

ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100

tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150

gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200

acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250

ttggtgtggt ctgacataaa taaataatct taaagcagct gttcccctcc 300

ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350

agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400

gatatttttg gaatgaaaag tttggggcct ttttagtaaa gtaaagaact 450

ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500

aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550

gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600

tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650

ttcatcaacc tccttttttt taaattttta ttctttttgg tatcaagatc 700

atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800

ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850

ataggtccta ggtttaacag ggccctattt gacccctgc ttgtggtgct 900

gctggctctt caacttcttg tggaggctgg tctggtgcgg gctcagacct 950

gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtggt 1000

cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050

gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100

agcacttgag gcacttgga atcctacagt tgagtaggaa ccatatcaga 1150

accattgaaa ttggggcttt caatggtctg gcgaacctca aactctgga 1200

actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

```



catggaaagc cacctgccca tgctgtctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcatgaa ccgttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750  
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacia 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1				5					10					15
Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

	155		160		165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp	410		415		420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
 620 625 630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
 635 640

&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

agccgacgct gctcaagctg caactctgtt gcagttggca gttcttttcg 50



gtttccctcc	tgctgtttgg	gggcatgaaa	gggcttcgcc	gccgggagta	100
aaagaaggaa	ttgaccgggc	agcgcgaggg	aggagcgcgc	acgcgaccgc	150
gagggcgggc	gtgcaccctc	ggctggaagt	ttgtgccggg	ccccgagcgc	200
gcgccggctg	ggagcttcgg	gtagagacct	aggccgctgg	accgcgatga	250
gcgcgccgag	cctccgtgcg	cgcgccgcgg	ggttggggct	gctgctgtgc	300
gcggtgctgg	ggcgcgctgg	ccggtccgac	agcggcggtc	gcggggaact	350
cgggcagccc	tctggggtag	ccgccgagcg	cccatgcccc	actacctgcc	400
gctgcctcgg	ggacctgctg	gactgcagtc	gtaagcggct	agcgcgtctt	450
cccgagccac	tcccgtcctg	ggtcgctcgg	ctggacttaa	gtcacaacag	500
attatctttc	atcaaggcaa	gttccatgag	ccaccttcaa	agccttcgag	550
aagtgaaact	gaacaacaat	gaattggaga	ccattccaaa	tctgggacca	600
gtctcggcaa	atattacact	tctctccttg	gctggaaaca	ggattgttga	650
aatactccct	gaacatctga	aagagtttca	gtcccttgaa	actttggacc	700
ttagcagcaa	caatatttca	gagctccaaa	ctgcatttcc	agccctacag	750
ctcaaatatc	tgtatctcaa	cagcaaccga	gtcacatcaa	tggaacctgg	800
gtattttgac	aatttggcc	acacactcct	tgtgttaaag	ctgaacagga	850
accgaatctc	agctatccca	cccaagatgt	ttaaactgcc	ccaactgcaa	900
catctcgaat	tgaaccgaaa	caagattaaa	aatgtagatg	gactgacatt	950
ccaaggcctt	ggtgctctga	agtctctgaa	aatgcaaaga	aatggagtaa	1000
cgaaacttat	ggatggagct	ttttgggggc	tgagcaacat	ggaaattttg	1050
cagctggacc	ataacaacct	aacagagatt	accaaaggct	ggctttacgg	1100
cttgctgatg	ctgcaggaac	ttcatctcag	ccaaaatgcc	atcaacagga	1150
tcagccctga	tgctggggag	ttctgccaga	agctcagtga	gctggacct	1200
actttcaatc	acttatcaag	gtagatgat	tcaagcttcc	ttggcctaag	1250
cttactaaat	acactgcaca	ttgggaacaa	cagagtcagc	tacattgctg	1300
attgtgcctt	ccgggggctt	tccagtttaa	agactttgga	tctgaagaac	1350

aatgaaatTT cctggactat tgaagacatg aatggTgctt tctctgggct 1400  
tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450  
ctaaaaaagc cttcactggT ttggatgcat tggagcatct agacctgagt 1500  
gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550  
actgcaacaa ttgcatttaa atacatcaag ccttttTgtgc gattgccagc 1600  
taaaatggct cccacagtgg gtggcgga aaactttca gagctttgta 1650  
aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcattttTgc 1700  
tgttagccca gatggctttg tgtgtgatga ttttcccaa cccagatca 1750  
cggttcagcc agaaacacag tcggcaataa aaggTtcaa tttgagTttc 1800  
atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttggaa 1850  
aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900  
tccggggcca aggtggcgag gtgatggagt ataccaccat ccttcggctg 1950  
cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctcaa 2000  
tcactttggT tcactctact ctgtcaaagc caagcttaca gtaaatatgc 2050  
ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100  
atggcacgct tggagtgtgc tgctgtgggg caccagccc cccagatagc 2150  
ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200  
tgcatgtgat gcccaggat gacgtgttct ttatcgtgga tgtgaagata 2250  
gaggacattg gggTatacag ctgcacagct cagaacagtg caggaagtat 2300  
ttcagcaaT gcaactctga ctgtcctaga aacaccatca tttttgcggc 2350  
cactgttTga ccgaactgta accaaggag aaacagccgt cctacagtgc 2400  
attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450  
cccattggTg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500  
tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550  
atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgtgat 2600  
cccactcca acctgcgact ccctcagat gacagcccca tcgttagacg 2650  
atgacggatg ggccactgtg ggtgtcgtga tcatagccgt ggtttgctgt 2700

gtgggtgggca cgtcactcgt gtgggtgggtc atcatatacc acacaaggcg 2750  
 gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800  
 cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850  
 gatgggtacg tgtcttcaga aagtggaaagc caccaccagt ttgtcacatc 2900  
 ttcagggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950  
 atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000  
 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050  
 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100  
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150  
 gagtgctacc catgttctca tccttcagaa gaatcctgcg aacggagctt 3200  
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250  
 actctcacia tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300  
 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350  
 ttctttcatg ggtaccttg gaaaagctct caggagacct cacctagatg 3400  
 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450  
 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500  
 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550  
 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600  
 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650  
 aacttttatt taaaagagag agaatcttat gttttttaaa tggagttatg 3700  
 aatttttaaaa ggataaaaaat gctttattta tacagatgaa ccaaaattac 3750  
 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800  
 ctttttaaac tattttttta ctttgtttta tgcaaaaaag tatcttacgt 3850  
 aaattaatga tataaatcat gattattttta tgtattttta taatgccaga 3900  
 tttcttttta tggaaaatga gttactaaag catttttaaat aataacctgcc 3950  
 ttgtaccatt ttttaaatag aagttacttc attatatttt gcacattata 4000

tttaataaaaa tgtgtcaatt tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4050

aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu  
1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly  
20 25 30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

	215		220		225
Lys Ile Lys Asn Val Asp Gly Leu Thr	Phe Gln Gly Leu Gly Ala				
230	235			240	
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met					
245	250			255	
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu					
260	265			270	
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly					
275	280			285	
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn					
290	295			300	
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu					
305	310			315	
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser					
320	325			330	
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn					
335	340			345	
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser					
350	355			360	
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile					
365	370			375	
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg					
380	385			390	
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala					
395	400			405	
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn					
410	415			420	
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys					
425	430			435	
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys					
440	445			450	
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln					
455	460			465	
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly					
470	475			480	

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	485	490	495
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	500	505	510
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	515	520	525
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	530	535	540
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	545	550	555
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	590	595	600
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	605	610	615
Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro	620	625	630
Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr	680	685	690
Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp	695	700	705
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala	710	715	720
Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser	725	730	735
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln	740	745	750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	755	760	765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	770	775	780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	785	790	795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	860	865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	875	880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	890	895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	920	925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	935	940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	995	1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu			

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe



<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 300  
gggtcttggt gaatgagg 18

<210> 301  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

ccccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 306

actccaagga aatcgatcc gttc 24

<210> 307

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 308

actccaagga aatcgatcc gttc 24

<210> 309

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 309

gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

caaaacttgc gtcgcggaga gcgcccagct tgacttgaat ggaaggagcc 50

cgagcccgcg gagcgcagct gagactgggg gagcgcgttc ggctgtggg 100

gcgcccgtcg gcgcccgggc gcagcaggga aggggaagct gtggtctgcc 150

ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200

ccgtccccta tccctccttt atatagaaac cttccacact gggaaaggcag 250

cggcgaggca ggagggctca tggtagcaa ggaggccggc tgatctgcag 300

gcgcacagca ttccgagttt acagatTTTT acagatacca aatggaaggc 350

gaggaggcag aacagcctgc ctggttccat cagccctggc gcccaggcgc 400



gccttcgcga agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750  
 gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800  
 tcaagcgcaa tgagctggct gccttggcac gaggggctcg ggcgggcatg 1850  
 gctcagctgc gtgagctgta cctcaccagc aaccgactgc gcagccgagc 1900  
 cctgggcccc cgtgcctggg tggacctcgc ccatctgcag ctgctggaca 1950  
 tcgcgggaa tcagctcaca gagatccccg aggggctccc cgagtcactt 2000  
 gagtacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050  
 cttcgactcc acgccccacc tcaaggggat ctttctcagg tttacaagc 2100  
 tggctgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150  
 caggtcttgg acattgaagg caacttagag ttggtgaca tttccaagga 2200  
 ccgtggccgc ttggggaagg aaaaggagga ggaggaagag gaggaggagg 2250  
 aggaagagga aacaagatag tgacaagggtg atgcagatgt gacctaggat 2300  
 gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350  
 cccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400  
 tcccacatga cacgggctga cacagtctca tatccccacc ccttcccacg 2450  
 gcgtgtccca cggccagaca catgcacaca catcacacc tcaaaccacc 2500  
 agctcagcca cacacaacta cctccaaac caccacagtc tctgtcacac 2550  
 cccactacc gctgccacgc cctctgaatc atgcaggga gggctctgcc 2600  
 ctgccctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650  
 tgcgatatga tacacaccac acacacacac atgcacaagt catgtgcgaa 2700  
 cagccctcca aagcctatgc cacagacagc tcttgcccca gccagaatca 2750  
 gccatagcag ctgcgcgtct gccctgtcca tctgtccgtc cgttccctgg 2800  
 agaagacaca agggatatca tgctctgtgg ccagggtgcct gccaccctct 2850  
 ggaactcaca aaagctggct ttatttcctt tccatccta tggggacagg 2900  
 agccttcagg actgctggcc tggcctggcc caccctgctc ctccagggtc 2950  
 tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000  
 caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100  
 ctgggctgag ccagggagga aggaccagc tgcacctagg agacaccttt 3150  
 gttcttcagg cctgtggggg aagtccggg tgcctttatt tttattctt 3200  
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250  
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 311  
 gcattggccg cgagactttg cc 22

<210> 312  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 312  
 gcggccacgg tccttggaat tg 22

<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 313  
 tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314  
 <211> 3003  
 <212> DNA  
 <213> Homo Sapien

<400> 314  
 gggagggggc tccggggcgc gcgcagcaga cctgctccgg ccgcgcgcct 50  
 cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100



gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450  
 gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500  
 gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550  
 gggacctgtg cctgtcattc aggcacaagg tgacggggct gcactctggc 1600  
 acactccagg tgtttgtgag aaaacacggg gccacaggag cagccctgtg 1650  
 gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700  
 gggctgacat caagagcgaa tcacaaagat gattaaaggg ttggaaaaaa 1750  
 agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800  
 agaagactga ggggcaaacc attgatgggt ttcaagtata tgaagggttg 1850  
 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900  
 caagagggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950  
 ggccattgtt agaatacttc ataaaaaag aagtgtgaaa atctcagtat 2000  
 ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggg 2050  
 taaagatgtt cttacccaag gaaaagtaac aaattataga atttcccaaa 2100  
 agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150  
 taatttggac aaggcttaat ttaggcattt cctctttgac ctctaattgg 2200  
 agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250  
 tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300  
 tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350  
 cctagtgtgg cggtggtttt caatgtttct tcatggtaaa ggtataagcc 2400  
 tttcatttgt tcaatggatg atgtttcaga tttttttttt ttttaagagat 2450  
 ctttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500  
 cttcgtgtgt gacaagtat cttggctgct gagaaagagt gccctgcccc 2550  
 acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600  
 tcaattggac tctcccagg tccacagaac agtaatat tttgaacaat 2650  
 aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggtgg 2700  
 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750



gtagatccat ttttaatggg tcatttcctt tatgggcata taactgcaca 2800  
gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850  
tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
catcttggtt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000  
aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu	1	5	10	15
Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val	20	25	30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys	170	175	180
Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys	185	190	195
Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr	200	205	210
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys	215	220	225
Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys	230	235	240
Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr	245	250	255
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro	260	265	270
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn	275	280	285
Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro	290	295	300
Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr	305	310	315
Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro	320	325	330
Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr	335	340	345
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala	350	355	360
Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln	365	370	375
Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val	380	385	390
His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu	395	400	405
Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly	410	415	420
Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys			

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly	Arg Leu Met His Ser Gly	
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys	Val Thr Gly Leu His Ser	
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys	His Gly Ala His Gly Ala	
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His	Gly Trp Arg Gln Thr Gln	
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys	Ser Glu Ser Gln Arg	
500	505	

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggacccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

<400> 319

cttcttttgaa	aaggattatc	acctgatcag	gttctctctg	catttgcccc	50
tttagattgt	gaaatgtggc	tcaaggtctt	cacaactttc	ctttcctttg	100
caacaggtgc	ttgctcgggg	ctgaaggtga	cagtgccatc	acacactgtc	150
catggcgta	gaggtcaggc	cctctaccta	cccgccact	atggcttcca	200
cactccagca	tcagacatcc	agatcatatg	gctatttgag	agaccccaca	250
caatgcccaa	atacttactg	ggctctgtga	ataagtctgt	ggttcctgac	300
ttggaatacc	aacacaagtt	caccatgatg	ccacccaatg	catctctgct	350
tatcaaccce	ctgcagttcc	ctgatgaagg	caattacatc	gtgaaggtca	400
acattcaggg	aaatggaact	ctatctgcca	gtcagaagat	acaagtcacg	450
gttgatgatc	ctgtcacaaa	gccagtgggt	cagattcatc	ctccctctgg	500
ggctgtggag	tatgtgggga	acatgaccct	gacatgccat	gtggaagggg	550
gcactcggct	agcttaccaa	tggctaaaaa	atgggagacc	tgtccacacc	600
agctccacct	actccttttc	tccccaaaac	aatacccttc	atattgctcc	650
agtaaccaag	gaagacattg	ggaattacag	ctgcctgggt	aggaaccctg	700
tcagtgaaat	ggaaagtgat	atcattatgc	ccatcatata	ttatggacct	750
tatggacttc	aagtgaattc	tgataaaggg	ctaaaagtag	gggaagtgtt	800
tactgttgac	cttgagagg	ccatcctatt	tgattgttct	gctgattctc	850
atccccccaa	cacctactcc	tggattagga	ggactgacaa	tactacatat	900
atcattaagc	atgggcctcg	cttagaagtt	gcctctgaga	aagtagccca	950
gaagacaatg	gactatgtgt	gctgtgctta	caacaacata	accggcaggc	1000
aagatgaaac	tcatttcaca	gttatcatca	cttccgtagg	actggagaag	1050
cttgcacaga	aaggaaaatc	attgtcacct	ttagcaagta	taactggaat	1100
atcactattt	ttgattatat	ccatgtgtct	tctcttccta	tggaaaaaat	1150
atcaacccta	caaagttata	aaacagaaac	tagaaggcag	gccagaaaca	1200
gaatacacga	aagctcaaac	attttcaggc	catgaagatg	ctctggatga	1250

ctctcggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300  
 ggattccaag caggtctggt ccagcctctg attgtgtatc ggggcaagat 1350  
 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400  
 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450  
 ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaactctg 1500  
 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
 tgcagaatag aggcatttat gcaaattgaa ctgcagggtt ttcagcatat 1600  
 acacaatgtc ttgtgcaaca gaaaaacatg ttgggggaaat attcctcagt 1650  
 ggagagtcgt tctcatgctg acgggggagaa cgaaagtgc aggggtttcc 1700  
 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750  
 acactttcac tatcatcaac actgagacta tctgtctca cctacaaatg 1800  
 tggaaacttt acattgttcg atttttcagc agactttggt ttattaaatt 1850  
 tttattagtg ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
 ttctatcttg ttatttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950  
 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100  
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15

Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro His Thr Met	Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser	65	70	75
Val Val Pro Asp	Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro	80	85	90
Pro Asn Ala Ser	Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu	95	100	105
Gly Asn Tyr Ile	Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu	110	115	120
Ser Ala Ser Gln	Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr	125	130	135
Lys Pro Val Val	Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr	140	145	150
Val Gly Asn Met	Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg	155	160	165
Leu Ala Tyr Gln	Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser	170	175	180
Ser Thr Tyr Ser	Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala	185	190	195
Pro Val Thr Lys	Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg	200	205	210
Asn Pro Val Ser	Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile	215	220	225
Tyr Tyr Gly Pro	Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu	230	235	240
Lys Val Gly Glu	Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu	245	250	255
Phe Asp Cys Ser	Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp	260	265	270
Ile Arg Arg Thr	Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro	275	280	285
Arg Leu Glu Val	Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp	290	295	300
Tyr Val Cys Cys	Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu	305	310	315
Thr His Phe Thr	Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu			

	320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly	335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp	350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly	365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His	380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe	395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro	410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr	425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu	440	445	450

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gacacctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcttcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

&lt;210&gt; 324

&lt;211&gt; 2397

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50

cctgggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgct aaaatcttca 200

accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttata 300

ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400

aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450

gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500

gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550

catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600

ctctgtatga tatttggtgc agattgcctt tgtccttcaa aaaggcgcag 650

accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700

aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatggt 750

tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800

gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950

ttgcagggtt cagtctagat tgctattaaa ttgaagagtc tacattcaga 1000

1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
 50  
 0



acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
 gatgggtttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
 atttatgtat atttggttaa taataaccta tttcaagtct gagttttgaa 1150  
 aatttacatt tccaagtat tgcattattg aggtatttaa gaagattatt 1200  
 ttagagaaaa atatttctca tttgatataa ttttctctg tttcactgtg 1250  
 tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300  
 agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
 caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
 attaattaat tacagttttc tacacatggg aatacaggat atgctactga 1450  
 tttaggaagt ttttaagttc atgggtattct cttgattcca acaaagtttg 1500  
 atttctctct gtatttttct tacttactat gggttacatt ttttattttt 1550  
 caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600  
 tatttttttg ttgtttcaaa ctgaagttta ctgagagatc catcaaattg 1650  
 aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700  
 cattcttgct gaacttcaac ttgaaattgt ttttttttcc tttttggatg 1750  
 tgaaggtgaa cattcctgat ttttgtctga tgtgaaaaag ccttgggtatt 1800  
 ttacattttg aaaattcaaa gaagcttaat ataaaagttt gcattctact 1850  
 caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900  
 atacagaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950  
 aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000  
 tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
 gtaggatgga acattttagt gtatttttac tccttaaaga gctagaatac 2100  
 atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150  
 ctgaccatta cgtagtagac aatttctgta atgtcccctt ctttctaggc 2200  
 tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250  
 ttcttttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
 tttggatgtg taacttgtga tgccttagaa aaatatccta agcacaaaat 2350

```
<210> 325
<211> 280
<212> PRT
```

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
1				5					10					15
Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
				20					25					30
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
				35					40					45
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
				50					55					60
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
				65					70					75
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
				80					85					90
Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
				95					100					105
Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
				110					115					120
Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
				125					130					135
Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
				140					145					150
Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
				155					160					165
His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
				170					175					180
Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
				185					190					195
Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
				200					205					210
Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu

215										220					225				
Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu					
				230					235					240					
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu					
				245					250					255					
Gly	Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser					
				260					265					270					
Leu	Gly	Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser										
				275					280										

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcagggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgc ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgtaa taattcaaca 50  
 aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100  
 ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150  
 acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
 cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
 agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350  
 ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
 tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450  
 agactggcct gcgctggagg accttgtcct gcaggactca gctgcagggt 500  
 ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550  
 gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600  
 ggaccacaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
 caatgctgag tgtggatgac tgctttggga tgggccgctc ggcctacaat 700  
 gaaggggact attatcatatc ggtgttgtgg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
 acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850  
 ctcacccgcc gcctgctctc ccttgaccca agccacgaac gagctggagg 900  
 gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950  
 taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
 aggctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050  
 tggggagggt gtcaaaactga cccccgtag acagaaggagg cttttctgta 1100  
 ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150  
 gaggaggacg agtgggacag cccgcacatc gtcaggtaact acgatgtcat 1200  
 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
 cagagccac cgttcgtgat cccaagacag gagtcctcac tgctgccagc 1300  
 taccgggttt ccaaagctc ctggctagag gaagatgatg accctgttgt 1350  
 ggcccagta aatcgctcga tgcagcatat cacagggtta acagtaaaga 1400  
 ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450  
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaaacaga 1500  
 ggggaatagg ttagcgacgt ttcttaacta catgagtgat gtagaagctg 1550  
 gtgggtgccac cgtcttcctt gatctggggg ctgcaatttg gcctaagaag 1600  
 ggtacagctg tgttctggta caacctcttg cggagcgggg aagtgacta 1650  
 ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700  
 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggtga 1750  
 tcaacagaag ttgactgaca tccttttctg tccttccctt tcctggctct 1800  
 tcagcccatg tcaacgtgac agacaccttt gtatgttcct ttgtatgttc 1850  
 ctatcaggct gatttttgga gaaatgaatg tttgtctgga gcagaggagg 1900  
 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
 gcctgtgcca tcctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
 gttagctgtc tagcgcttag caaggctgct ttgtacctca ggtgttttag 2050  
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg cattttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val	1	5	10	15
Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met	20	25	30	
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys	35	40	45	
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser	50	55	60	
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75	
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90	
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105	
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg	110	115	120	
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala	125	130	135	
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile	140	145	150	
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165	
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180	
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195	
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210	

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe



<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

<400> 338  
gcagtattga gttttacttc ctctctttt tagtggaga cagaccataa 50  
tcccagtgat agtgaaattg attgtttcat ttattaccgt tttggctggg 100  
ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gacccaggt tctctggta aaactgaaag 250  
cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300  
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400  
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
cccctactac agggacccca acaagcccta caagaagggtg ctgaggactc 600  
ggtacatcca gacagagctg ggctcccgtg agcgggttgc ggtggctgtc 650  
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
ggtggcccat cacttccctc ggttactcta cttcactggg cagcgggggg 750  
cccgggctcc agcagggatg caggtggtgt ctcattggga tgagcggccc 800

gcctggctca	tgtcagagac	cctgcgccac	cttcacacac	actttggggc	850
cgactacgac	tggttcttca	tcatgcagga	tgacacatat	gtgcaggccc	900
cccgcctggc	agcccttgct	ggccacctca	gcaccaacca	agacctgtac	950
ttaggccggg	cagaggagtt	cattggcgca	ggcgagcagg	cccggtactg	1000
tcatgggggc	tttggctacc	tgttgtcacg	gagtctcctg	cttcgtctgc	1050
ggccacatct	ggatggctgc	cgaggagaca	ttctcagtgc	ccgtcctgac	1100
gagtggcttg	gacgctgcct	cattgactct	ctgggcgtcg	gctgtgtctc	1150
acagcaccag	gggcagcagt	atcgctcatt	tgaactggcc	aaaaataggg	1200
accctgagaa	ggaagggagc	tcggctttcc	tgagtgcctt	cgccgtgcac	1250
cctgtctccg	aaggtaccct	catgtaccgg	ctccacaaac	gcttcacgcg	1300
tctggagttg	gagcgggctt	acagtgaaat	agaacaactg	caggctcaga	1350
tccggaacct	gaccgtgctg	acccccgaag	gggaggcagg	gctgagctgg	1400
cccgttgggc	tccctgctcc	tttcacacca	cactctcgct	ttgaggtgct	1450
gggctgggac	tacttcacag	agcagcacac	cttctcctgt	gcagatgggg	1500
ctcccaagtg	cccactacag	ggggctagca	gggcggacgt	gggtgatgcg	1550
ttggagactg	ccctggagca	gctcaatcgg	cgctatcagc	ccgcctgcg	1600
cttcacagaag	cagcgactgc	tcaacggcta	tcggcgcttc	gaccacgcac	1650
ggggcatgga	gtacacctcg	gacctgctgt	tggaatgtgt	gacacagcgt	1700
gggcaccggc	gggccctggc	tcgcagggtc	agcctgctgc	ggccactgag	1750
ccgggtggaa	atcctacctc	tgcctatgt	cactgaggcc	acccgagtgc	1800
agctggtgct	gccactcctg	gtggctgaag	ctgctgcagc	ccgggctttc	1850
ctcgaggcgt	ttgcagccaa	tgtcctggag	ccacgagaac	atgcattgct	1900
cacctgttg	ctggtctacg	ggccacgaga	aggtggccgt	ggagctccag	1950
accattttct	tggggtgaag	gctgcagcag	cggagttaga	gcgacggtac	2000
cctgggacga	ggctggcctg	gctcgctgtg	cgagcagagg	ccccttccca	2050
ggtgcgactc	atggacgtgg	tctcgaagaa	gcacctgtg	gacactctct	2100

tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150  
 tgtcgcatga atgccatctc tggtggcag gccttctttc cagtccattt 2200  
 ccaggagttc aatcctgccc tgtcaccaca gagatcaccc ccaggggccc 2250  
 cgggggctgg cctgacccc ccctcccctc ctggtgctga cccctcccgg 2300  
 ggggctccta taggggggag atttgaccgg caggettctg cggagggctg 2350  
 cttctacaac gctgactacc tggcggcccg agcccggctg gcagggtgaac 2400  
 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450  
 gttttcctcc ggttctcagg gctccacctc tttcgggccc tagagccagg 2500  
 gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcaagtgaag 2550  
 aactctacca ccgctgccgc ctcaagcaacc tggaggggct agggggccgt 2600  
 gccagctgg ctatggctct ctttgagcag gacgaggcca atagcactta 2650  
 gcccgctgg gggccctaac ctcattacct ttcctttgtc tgccctcagcc 2700  
 ccaggaaggg caaggcaaga tggcggacag atagagaatt gttgctgtat 2750  
 tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
1				5					10					15

Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
			20						25					30

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
				35					40					45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
				50					55					60

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
				65					70					75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
				80					85					90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				95					100					105
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val
				110					115					120
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr
				125					130					135
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser
				140					145					150
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg
				155					160					165
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile
				170					175					180
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu
				185					190					195
Ala	Gly	His	Leu	Ser	Ile	Asn	Gln	Asp	Leu	Tyr	Leu	Gly	Arg	Ala
				200					205					210
Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly
				215					220					225
Gly	Phe	Gly	Tyr	Leu	Leu	Ser	Arg	Ser	Leu	Leu	Leu	Arg	Leu	Arg
				230					235					240
Pro	His	Leu	Asp	Gly	Cys	Arg	Gly	Asp	Ile	Leu	Ser	Ala	Arg	Pro
				245					250					255
Asp	Glu	Trp	Leu	Gly	Arg	Cys	Leu	Ile	Asp	Ser	Leu	Gly	Val	Gly
				260					265					270
Cys	Val	Ser	Gln	His	Gln	Gly	Gln	Gln	Tyr	Arg	Ser	Phe	Glu	Leu
				275					280					285
Ala	Lys	Asn	Arg	Asp	Pro	Glu	Lys	Glu	Gly	Ser	Ser	Ala	Phe	Leu
				290					295					300
Ser	Ala	Phe	Ala	Val	His	Pro	Val	Ser	Glu	Gly	Thr	Leu	Met	Tyr
				305					310					315
Arg	Leu	His	Lys	Arg	Phe	Ser	Ala	Leu	Glu	Leu	Glu	Arg	Ala	Tyr
				320					325					330
Ser	Glu	Ile	Glu	Gln	Leu	Gln	Ala	Gln	Ile	Arg	Asn	Leu	Thr	Val
				335					340					345
Leu	Thr	Pro	Glu	Gly	Glu	Ala	Gly	Leu	Ser	Trp	Pro	Val	Gly	Leu
				350					355					360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	
				365					370					375	
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	
				380					385					390	
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	
				395					400					405	
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	
				410					415					420	
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	
				425					430					435	
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	
				440					445					450	
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	
				455					460					465	
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	
				470					475					480	
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	
				485					490					495	
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	
				500					505					510	
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	
				515					520					525	
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	
				530					535					540	
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	
				545					550					555	
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	
				560					565					570	
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	
				575					580					585	
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	
				590					595					600	
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	
				605					610					615	
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	
				620					625					630	

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
 770

&lt;210&gt; 340

&lt;211&gt; 1572

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 340

cggagtggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50  
 tgtccccaag ccgttctaga cgcggaagaa atgctttctg aaagcagctc 100  
 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatattctga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

```
<210> 341
<211> 318
<212> PRT
<213> Homo Sapien
```

&lt;400&gt; 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly	1	5	10	15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile	20	25	30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys				



	260		265		270									
Cys	Ser	Asp	Met	Ala	Val	Thr	Phe	Asn	Gly	Leu	Thr	Pro	Asn	Gln
			275						280					285
Met	His	Val	Met	Met	Tyr	Gly	Val	Tyr	Arg	Leu	Arg	Ala	Phe	Gly
			290						295					300
His	Ile	Phe	Asn	Asp	Ala	Leu	Val	Phe	Leu	Pro	Pro	Asn	Gly	Ser
			305						310					315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatac gactcact atagggtca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggtgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 350  
ggattctaatac gactcact atagggcggc gatgtccact ggggctac 48

<210> 351  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 351  
ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatggt 48

<210> 352  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 352  
ggattctaatac gactcact atagggcacc cacgcgtccg gctgctt 47

<210> 353  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 353  
ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48

<210> 354  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 354  
ggattctaatac gactcact atagggcttg ctgcggtttt tggtcctg 48

<210> 355  
<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 355

ctatgaaatt aaccctcact aaaggagct gccgatccca ctggtatt 48

<210> 356

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 356

ggattctaatac gactcact atagggcgga tcctggccgg cctctg 46

<210> 357

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 357

ctatgaaatt aaccctcact aaaggagcc cgggcatggt ctcagtta 48

<210> 358

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

ggattctaatac gactcact atagggcggg aagatggcga ggaggag 47

<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 359

ctatgaaatt aaccctcact aaaggaccca aggccacaaa cggaaatc 48

<210> 360  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 360  
ggattctaatac gactcact atagggctgt gctttcattc tgccagta 48

<210> 361  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 361  
ctatgaaatt aaccctcact aaaggaggagg tacaattaag gggtaggat 48

<210> 362  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 362  
ggattctaatac gactcact atagggcccg cctcgctcct gctcctg 47

<210> 363  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaatt aaccctcact aaaggaggga ttgccgcgac cctcacag 48

<210> 364  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 364

ggatttctaatac gactcact atagggcccc tctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaatt aaccctcact aaaggagtg gtggccgcga ttatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggatttctaatac gactcact atagggcgca gcatggcag cgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaatt aaccctcact aaaggacag acggggcaga gggagtg 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggatttctaatac gactcact atagggccag gaggcgtgag gagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatacgcactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatacgcactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaatac gactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc acaaaaacac tcctgaggag aaagaaagag 50

agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100

aaaaaatgaa ttcattctaaa tcatctgaaa cacaatgcac agagagagga 150

tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200

atttctcagt gcctgtttca tcaccagatg tggtgtgaca tttcgcattc 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctcctgct acaattatgg atcagggtca gtcaagaatt gttgtccatt 350

gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400

tttctctggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450

gtgggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggc 550

agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600

gatgtagggg agcccaacaa catagctacc ctggaggact gtgcccacat 650

gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700

tcaattatct tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750



ggaaaaatctc ttttaagaaca gaaggcacaa ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly	1	5	10	15
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	20	25	30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	35	40	45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	50	55	60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	65	70	75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	80	85	90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	95	100	105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	110	115	120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	125	130	135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	140	145	150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	155	160	165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	170	175	180	

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
 215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcttacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

<210> 382  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
ggccttgacg acaaccgt 18

<210> 383  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 384  
cagctgccct tccccaacca 20

<210> 385  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 385  
catcaagcgc ctctacca 18

<210> 386  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386

cacaaactcg aactgcttct g 21

<210> 387

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

gggccatcac agctccct 18

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gggatgtggt gaacacagaa ca 22

<210> 389

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 389

tgccagctgc atgctgccag tt 22

<210> 390

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggctttggta gt 22

<210> 398  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc cccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 400  
gcaaattcag ggctcactag aga 23

<210> 401  
<211> 29

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 401  
cacagagcat ttgtccatca gcagttcag 29

<210> 402  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 402  
ggcagagact tccagtcact ga 22

<210> 403  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 403  
gccaaaggggtg gtgtagata gg 22

<210> 404  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
caggccccct tgatctgtac ccca 24

<210> 405  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 405  
gggacgtgct tctacaagaa cag 23

<210> 406  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
caggcttaca atgttatgat cagaca 26

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
tattcagagt tttccattgg cagtgccagt t 31

<210> 408  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
tctacatcag cctctctgcg c 21

<210> 409  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 409  
cgatcttctc caccaggag cgg 23

<210> 410  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 410



gccaggcctc acattcgt 18

<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

ctccctgaat ggcagcctga gca 23

<210> 412

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

aggtgtttat taagggccta cgct 24

<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cagagcagag ggtgccttg 19

<210> 414

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 414

tggcggagtc ccctcttggc t 21

<210> 415

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaacccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 420

tgtctgcctc agccccagga agg 23

<210> 421

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atcttgcctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

gggactacaa gccgcgccgc gctgccgctg gccctcagc aaccctcgac 50  
atggcgctga ggcgccacc gcgactccgg ctctgcgctc ggctgcctga 100  
cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
tcaaatccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
ctgtcttgca tcattacgga ttgcagaca agtgacccca ggatcgagt 250  
gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450  
ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500  
ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600  
ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650  
acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700  
ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt	ctatgacctg	aacattggcg	gaattattgg	ggggggttctg	800
gttgccttg	ctgtactggc	cctgatcacg	ttgggcatct	gctgtgcata	850
cagacgtggc	tacttcatca	acaataaaca	ggatggagaa	agttacaaga	900
accaggggaa	accagatgga	gttaactaca	tccgcactga	cgaggagggc	950
gacttcagac	acaagtcatc	gtttgtgatc	tgagacccgc	ggtgtggctg	1000
agagcgcaca	gagcgcacgt	gcacatacct	ctgctagaaa	ctcctgtcaa	1050
ggcagcgaga	gctgatgcac	tccgacagag	ctagacactc	attcagaagc	1100
ttttcgtttt	ggccaaagtt	gaccactact	cttcttactc	taacaagcca	1150
catgaataga	agaattttcc	tcaagatgga	cccggtaa	ataaccacaa	1200
ggaagcgaaa	ctgggtgcgt	tactgagtt	gggttcctaa	tctgtttctg	1250
gcctgattcc	cgcattgagta	ttagggatgat	cttaaagagt	ttgctcacgt	1300
aaacgcccgt	gctgggccct	gtgaagccag	catgttcacc	actggtcggt	1350
cagcagccac	gacagcacca	tgtgagatgg	cgagggtggct	ggacagcacc	1400
agcagcgcac	cccgccggga	accagaaaa	ggcttcttac	acagcagcct	1450
tacttcacgt	gcccacagac	accaccgcag	tttcttctta	aaggctctgc	1500
tgatcggtgt	tgcagtgtcc	attgtggaga	agcttttttg	atcagcattt	1550
tgtaaaaaaca	acccaaatca	ggaaggtaaa	ttggttgctg	gaagagggat	1600
cttgctgag	gaacctgtct	tgtccaacag	ggtgtcagga	tttaaggaaa	1650
accttcgtct	taggctaagt	ctgaaatgg	actgaaatat	gcttttctat	1700
gggtcttggt	tattttataa	aattttacat	ctaaattttt	gctaagggat	1750
tattttgatt	attgaaaaga	aaatttctat	ttaaactgta	aatatattgt	1800
catacaaatgt	taaataacct	atTTTTTTTaa	aaaagttcaa	cttaaggtag	1850
aagttccaag	ctactagtgt	taaattggaa	aatatcaata	attaagagta	1900
ttttacccaa	ggaatcctct	catggaagtt	tactgtgatg	ttccttttct	1950
cacacaagtt	ttagcctttt	tcacaaggga	actcatactg	tctacacatc	2000
agaccatagt	tgttaggaa	accttttaaaa	attccagtta	agcaatgttg	2050

aaatcagttt	gcattctctt	aaaagaaacc	tctcaggtta	gctttgaact	2100
gcctcttcct	gagatgacta	ggacagctctg	taccagaggg	ccaccagaa	2150
gccctcagat	gtacatacac	agatgccagt	cagctcctgg	ggttgcgcca	2200
ggcgcccccg	ctctagctca	ctggtgcctc	gctgtctgcc	aggaggccct	2250
gccatccttg	ggccctggca	gtggctgtgt	cccagtgagc	tttactcacg	2300
tggcccttgc	ttcatccagc	acagctctca	ggtgggcact	gcagggacac	2350
tgggtgtcttc	catgtagcgt	cccagctttg	ggctcctgta	acagacctct	2400
ttttggttat	ggatggctca	caaaataggg	cccccaatgc	tatttttttt	2450
ttttaagttt	gtttaattat	ttgttaagat	tgtctaaggc	caaaggcaat	2500
tgcgaaatca	agtctgtcaa	gtacaataac	atttttaaaa	gaaaatggat	2550
cccactgttc	ctctttgcc	cagagaaagc	accagacgc	cacaggctct	2600
gtcgcatttc	aaaacaaacc	atgatggagt	ggcggccagt	ccagcctttt	2650
aaagaacgtc	aggtggagca	gccaggtgaa	aggcctggcg	gggaggaaag	2700
tgaaacgcct	gaatcaaaag	cagttttcta	attttgactt	taaatttttc	2750
atccgcggga	gacaactgctc	ccatttgtgg	ggggacatta	gcaacatcac	2800
tcagaagcct	gtgtttcttca	agagcaggtg	ttctcagcct	cacatgccct	2850
gccgtgctgg	actcaggact	gaagtgctgt	aaagcaagga	gctgctgaga	2900
aggagcactc	cactgtgtgc	ctggagaatg	gctctcacta	ctcaccttgt	2950
ctttcagctt	ccagtgtctt	gggtttttta	tactttgaca	gctttttttt	3000
aattgcatac	atgagactgt	gttgactttt	tttagttatg	tgaaacactt	3050
tgccgcaggc	cgctggcgag	aggcaggaaa	tgctccagca	gtggctcagt	3100
gctccctggg	gtctgctgca	tggcatcctg	gatgcttagc	atgcaagttc	3150
cctccatcat	tgccaccttg	gtagagaggg	atggctcccc	accctcagcg	3200
ttggggattc	acgctccagc	ctccttcttg	gttgtcatag	tgatagggta	3250
gccttattgc	cccctcttct	tataccctaa	aaccttctac	actagtgcc	3300
tgggaaccag	gtctgaaaaa	gtagagagaa	gtgaaagtag	agtctgggaa	3350
gtagctgcct	ataactgaga	ctagacggaa	aaggaatact	cgtgtatttt	3400

```
<210> 423
<211> 310
<212> PRT
<213> Homo Sapien
```

<400> 423														
Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu
1				5					10					15
Pro	Asp	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly
				20					25					30
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35					40					45
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50					55					60
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr
				65					70					75
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
				80					85					90
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
				95					100					105
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
				110					115					120
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
				125					130					135
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
				140					145					150
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly
				155					160					165
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
				170					175					180
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
				185					190					195

His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
				200					205					210
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
				215					220					225
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
				230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
				245					250					255
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100